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Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

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STIC-Biotech/ChemLib

104375

From: Slobodyansky, Elizabeth
Sent: Tuesday, September 23, 2003 6:42 PM
To: STIC-Biotech/ChemLib
Subject: 09/974,973

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Please search for case 09/974,973

20

SEQ ID NOs: 2 and 19 against commercial ~~and interference~~ databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner

Art Unit 1652
CM1 10D11
703-306-3222

mail box 10D01

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 9/25/03
Date Completed: 9/25/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: ✓
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: ✓
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

XX 12-OCT-2001; 2001WO-US31893.
 XX
 XX
 PR 13-OCT-2000; 2000US-239913P.
 XX
 XX (ARCH) ARCHER-DANIELS MIDLAND CO.
 XX
 XX Hanke PD;
 XX
 XX WPI: 2002-463267/49.
 DR N-PSDB; ABK52832.
 XX
 PT Novel mutated, feedback resistant pyruvate carboxylase enzyme
 PT polypeptide, useful for producing amino acids e.g. L-lysine,
 PT L-threonine, L-glycine, L-glutamic acid, L-proline and L-methionine and
 PT L-isoleucine
 XX
 PS Claim 17; Fig 1; 42pp; English.
 XX
 CC The present invention relates to a new mutated, feedback-resistant
 CC pyruvate carboxylase enzyme. The invention is useful for producing an
 CC amino acid (e.g. L-Lys, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro),
 CC by culturing a host cell in a suitable media and separating the amino
 CC acid from the medium. The vector of the invention is useful for
 CC replacement of a wild-type pyruvate carboxylase gene, with a feedback
 CC resistant pyruvate carboxylase gene, in a Corynebacterium glutamicum, by
 CC replacing a genomic copy of the wild-type pyruvate carboxylase gene with
 CC a selectable marker gene through homologous recombination to form a first
 CC recombination strain, and replacing the selectable marker gene in the
 CC first recombinant strain, with feedback resistant pyruvate carboxylase
 CC gene through homologous recombination to form a second recombinant
 CC strain, where the homologous recombination in the above steps, occurs
 CC between the host cell and the vector. The feedback-resistant pyruvate
 CC carboxylase enzyme is resistant to feedback inhibition from aspartic
 CC acid. The present amino acid sequence represents the feedback-resistant
 CC pyruvate carboxylase enzyme of the invention.
 XX
 SQ Sequence 1157 AA;
 Query Match 100.0%; Score 5865; DB 23; Length 1157;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTAITLGGLLGKIITLVSTHTSSTLPAPFKKILVANRGEIYVAFRAALETGAATVAIYP 60
 DB 1 MTAITLGGLLGKIITLVSTHTSSTLPAPFKKILVANRGEIYVAFRAALETGAATVAIYP 60
 QY 61 REDRGSFHRSEAFSEAVRIGTEGSPVKAYLDIDDEITGAAKKVRADATYPGYGLSENAQLA 120
 DB 61 REDRGSFHRSEAFSEAVRIGTEGSPVKAYLDIDDEITGAAKKVRADATYPGYGLSENAQLA 120
 QY 121 RECAENGITFIGTPEVLDTGDKSRNAVTAACKAGLPVLAESTPSKNIDDIYKSAEGQTY 180
 DB 121 RECAENGITFIGTPEVLDTGDKSRNAVTAACKAGLPVLAESTPSKNIDDIYKSAEGQTY 180
 QY 181 PIFVKAVAGGGGRMFVSSPDELRLKLAETASREAEAFDGSVYVERAVINPQHEVOI 240
 DB 181 PIFVKAVAGGGGRMFVSSPDELRLKLAETASREAEAFDGSVYVERAVINPQHEVOI 240
 QY 241 LGDRGTEVHVLRDCSLQRRHKQVVEIAPAOHLDELDRICADAVKFCRSIGYGAGT 300
 DB 241 LGDRGTEVHVLRDCSLQRRHKQVVEIAPAOHLDELDRICADAVKFCRSIGYGAGT 300
 QY 301 VEFLVDKGNHVFIEENPRIQVEHTVTEEVTDVLVKAQMRLAAGATLKELGLTDKIKT 360
 DB 301 VEFLVDKGNHVFIEENPRIQVEHTVTEEVTDVLVKAQMRLAAGATLKELGLTDKIKT 360
 QY 361 HGNAQCRIITDPNNGFPDGTITAYRSPGAGVRLDGAALGGEITAHFDSMLVKMT 420
 DB 361 HGNAQCRIITDPNNGFPDGTITAYRSPGAGVRLDGAALGGEITAHFDSMLVKMT 420
 QY 421 CRGSDPETAVARAQALAEFTVSGVATNIGFLRALIREEDFTSKRIATGFIGDHPHLLQA 480

DB 421 CRGSDPETAVARAQALAEFTVSGVATNIGFLRALIREEDFTSKRIATGFIGDHPHLLQA 480
 QY 481 PPADDEQGRILDYLDADVTYVKNKPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDRKLGPA 540
 DB 481 PPADDEQGRILDYLDADVTYVKNKPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDRKLGPA 540
 QY 541 FARDLREQDALAVTDTTFRDAHQSLIATRVRSFALKPAAEAVAKLTPELLSVEAMGGATY 600
 DB 541 FARDLREQDALAVTDTTFRDAHQSLIATRVRSFALKPAAEAVAKLTPELLSVEAMGGATY 600
 QY 601 DVAMRFLFEDPWDRDLDELREAMPNVIQMLLGRNTVGYTPYDPSVCRAFAVEAASSGYD 660
 DB 601 DVAMRFLFEDPWDRDLDELREAMPNVIQMLLGRNTVGYTPYDPSVCRAFAVEAASSGYD 660
 QY 661 IFRIFDALNDVSMRPAIDAVLETNTAVAEVAMAYSGDLSDFNEKLYLTDYLLKAAEIV 720
 DB 661 IFRIFDALNDVSMRPAIDAVLETNTAVAEVAMAYSGDLSDFNEKLYLTDYLLKAAEIV 720
 QY 721 KSGAHILAIKDMAGLLRPAAVTKLVTALRRREFDLPVHVHTHTAGGQATYFAAAQAGAD 780
 DB 721 KSGAHILAIKDMAGLLRPAAVTKLVTALRRREFDLPVHVHTHTAGGQATYFAAAQAGAD 780
 QY 781 AVDGASAPLSGTTSQPSLSAIVAAFAHTPRDTGLSLEAVSDLEPYWEAVRGILYLFESGT 840
 DB 781 AVDGASAPLSGTTSQPSLSAIVAAFAHTPRDTGLSLEAVSDLEPYWEAVRGILYLFESGT 840
 QY 841 PGPTGRVYRHEIPGGQSLNLRQAATAGLADRFELIEDNYAAVNEMLGRPTKVTPTSSKV 900
 DB 841 PGPTGRVYRHEIPGGQSLNLRQAATAGLADRFELIEDNYAAVNEMLGRPTKVTPTSSKV 900
 QY 901 GDALHLVGAGVDPADFAADPOKYDIPDSVIAFLRGELGNPPGGPPEPLRTRALGRSEG 960
 DB 901 GDALHLVGAGVDPADFAADPOKYDIPDSVIAFLRGELGNPPGGPPEPLRTRALGRSEG 960
 QY 961 KAPLFEVPEEQAHLDADDKSKERRNSLNRLLPKPTPEEFLHRRRFGNTSALDDREFFYG 1020
 DB 961 KAPLFEVPEEQAHLDADDKSKERRNSLNRLLPKPTPEEFLHRRRFGNTSALDDREFFYG 1020
 QY 1021 LVGRETILRLPDVRTPLLVRLDAISEPDDKGMNVVAVNNGIIRPMRVDRDSVESVTAT 1080
 DB 1021 LVGRETILRLPDVRTPLLVRLDAISEPDDKGMNVVAVNNGIIRPMRVDRDSVESVTAT 1080
 QY 1081 AKKADSSNKGHVAAPFAGVVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERY 1140
 DB 1081 AKKADSSNKGHVAAPFAGVVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERY 1140
 QY 1141 VPAATKVEGGDLIVVVS 1157
 DB 1141 VPAATKVEGGDLIVVVS 1157
 RESULT 2
 AAU98052
 ID AAU98052 standard; Protein; 1140 AA.
 XX
 AC AAU98052;
 XX
 XX 27-AUG-2002 (first entry)
 XX
 DE Corynebacterium mutant feedback-resistant pyruvate carboxylase enzyme.
 XX
 KW Feedback-resistant; pyruvate carboxylase; enzyme;
 KW aspartic acid feedback inhibition resistant; mutant; muten.
 XX
 OS Corynebacterium glutamicum.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "Wild-type Met substituted by Val"
 FT Misc-difference 153
 FT /note= "Wild-type Glu substituted by Asp"
 FT Misc-difference 182

FT Misc-difference /note= "Wild-type Ala substituted by Ser"
 FT 206
 FT /note= "Wild-type Ala substituted by Ser"
 FT 227
 FT /note= "Wild-type His substituted by Arg"
 FT 455
 FT /note= "Wild-type Ala substituted by Gly"
 FT 1110..1122
 FT /note= "Specifically claimed in claim 18"
 FT 1116
 FT /note= "Wild-type Asp substituted by Glu"
 FT 252
 PN WO200231158-A2.
 XX 18-APR-2002.
 XX 12-OCT-2001; 2001WO-US31893.
 XX 13-OCT-2000; 2000US-239913P.
 XX (ARCH) ARCHER-DANIELS MIDLAND CO.
 XX Hanke PD;
 XX WPI; 2002-463267/49.
 XX Novel mutated, feedback resistant pyruvate carboxylase enzyme
 PT polypeptide, useful for producing amino acids e.g. L-lysine,
 PT L-threonine, L-glycine, L-glutamic acid, L-proline and L-methionine and
 PT L-isoleucine
 XX Claim 1; Page -; 42pp; English.
 XX The present invention relates to a new mutated, feedback-resistant
 CC pyruvate carboxylase enzyme. The invention is useful for producing an
 CC amino acid (e.g. L-lys, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro),
 CC by culturing a host cell in a suitable media and separating the amino
 CC acid from the medium. The vector of the invention is useful for
 CC replacement of a wild-type pyruvate carboxylase gene, with a feedback
 CC resistant pyruvate carboxylase gene, in a Corynebacterium glutamicum, by
 CC replacing a genomic copy of the wild-type pyruvate carboxylase gene with
 CC a selectable marker gene through homologous recombination to form a first
 CC recombination strain, and replacing the selectable marker gene in the
 CC first recombinant strain, with feedback resistant pyruvate carboxylase
 CC gene through homologous recombination to form a second recombinant
 CC strain, where the homologous recombination in the above steps, occurs
 CC between the host cell and the vector. The feedback-resistant pyruvate
 CC carboxylase enzyme is resistant to feedback inhibition from aspartic
 CC acid. The present amino acid sequence represents the mutant
 CC feedback-resistant pyruvate carboxylase enzyme of the invention.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the wild-type feedback-resistant pyruvate carboxylase
 CC enzyme (AAU98053) given in figure 2 of the specification.
 XX
 SQ Sequence 1140 AA;
 Query Match 98.5%; Score 5779; DB 23; Length 1140;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1138; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 18 VSTHTSSTLPAPKKILVNRGEGIAVRAFAALTAETGAATVAIYPREDRGSFHSFSEAVR 77
 Db 1 VSTHTSSTLPAPKKILVNRGEGIAVRAFAALTAETGAATVAIYPREDRGSFHSFSEAVR 60
 QY 78 IGTEGSPVKAYLIDIDEIIGAARKKADAIYPGYGFSENAQLARECAENGIFIGTPTPV 137
 Db 61 IGTEGSPVKAYLIDIDEIIGAARKKADAIYPGYGFSENAQLARECAENGIFIGTPTPV 120
 QY 138 LDLTGDKSRVTAARKAGLPVLAESTPSKNIDDIIVKSAEGQYPIFVRAVAGGGGRGMRF 197
 Db 121 LDLTGDKSRVTAARKAGLPVLAESTPSKNIDDIIVKSAEGQYPIFVRAVAGGGGRGMRF 180
 QY 198 VSSPDELRLKATEASREAEAFDGSVYVERAVINPQHIEVQLDGRGTEVGHLYERDCS 257

Db 181 VSSPDELRLKATEASREAEAFDGSVYVERAVINPQHIEVQLDGRGTEVGHLYERDCS 240
 QY 258 LQRRHQKVVEIAPAOHLDPDLORICADAVKCRSIGYOGAGTVEFLVDEKGNHVEIEN 317
 Db 241 LQRRHQKVVEIAPAOHLDPDLORICADAVKCRSIGYOGAGTVEFLVDEKGNHVEIEN 300
 QY 318 PRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKLGLTQDKIKTHGAALOCRTTDPNNG 377
 Db 301 PRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKLGLTQDKIKTHGAALOCRTTDPNNG 360
 QY 378 FRPDTGTTAYRSPGAGVRLDGAOLGGEITTAHFDMSMLVKMTCRGSDPETAVARAQAL 437
 Db 361 FRPDTGTTAYRSPGAGVRLDGAOLGGEITTAHFDMSMLVKMTCRGSDPETAVARAQAL 420
 QY 438 AEFTVSGVATNIGFLRALLREDEFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYADV 497
 Db 421 AEFTVSGVATNIGFLRALLREDEFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYADV 480
 QY 498 TYNKPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDLKQLGPAFAFARDLREQDALAVTDT 557
 Db 481 TYNKPHGVRPKDVAAPIDKLPNIKDLPLPRGSRDLKQLGPAFAFARDLREQDALAVTDT 540
 QY 558 FRDAHQSLLATRVRSFALKPAAEAVALKLTPELLSVEANGGATYDVAMRFLFEDPDWRLDE 517
 Db 541 FRDAHQSLLATRVRSFALKPAAEAVALKLTPELLSVEANGGATYDVAMRFLFEDPDWRLDE 500
 QY 618 LREAMPNVNIOMLLGRNTVGTTPDPSVCRAFKVEAASSGVVDIFRIFDALNDVDSOMRPA 677
 Db 601 LREAMPNVNIOMLLGRNTVGTTPDPSVCRAFKVEAASSGVVDIFRIFDALNDVDSOMRPA 660
 QY 678 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYLTLDYLYLKMAEEIVKSGAHILAIXDMAGLLR 737
 Db 661 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYLTLDYLYLKMAEEIVKSGAHILAIXDMAGLLR 720
 QY 738 PAAVTKLVYALRRFEDLPVHVHTHTAGGOLATYFAAQAQADADVDGASAPISGTTSPQS 797
 Db 721 PAAVTKLVYALRRFEDLPVHVHTHTAGGOLATYFAAQAQADADVDGASAPISGTTSPQS 780
 QY 798 LSAIVAAAPAHTRDRTGLSLEAVSDLEPYWEAVRGVLYLPFESGTPGPTGVYRHEIPGGOL 857
 Db 781 LSAIVAAAPAHTRDRTGLSLEAVSDLEPYWEAVRGVLYLPFESGTPGPTGVYRHEIPGGOL 840
 QY 858 SNLRAQATAGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDIALHLVGAGVDPAF 917
 Db 841 SNLRAQATAGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDIALHLVGAGVDPAF 900
 QY 918 AADPKYDIPDSVIAFLRGELGNPPGGWPEPLTRALEGRSGKAPLTVPEEQAHLLDA 977
 Db 901 AADPKYDIPDSVIAFLRGELGNPPGGWPEPLTRALEGRSGKAPLTVPEEQAHLLDA 960
 QY 978 DDSKERRNSLNRLFPKPTPEEFLEHRRRFGNTSALDDREFFYGLVEGRETLRLPDVRTP 1037
 Db 961 DDSKERRNSLNRLFPKPTPEEFLEHRRRFGNTSALDDREFFYGLVEGRETLRLPDVRTP 1020
 QY 1038 LLVRDLDAISEPDDKGMNRNVVANNVNGQIRPMRVDRDSVESVATAEKADSSNGHVAAPFA 1097
 Db 1021 LLVRDLDAISEPDDKGMNRNVVANNVNGQIRPMRVDRDSVESVATAEKADSSNGHVAAPFA 1080
 QY 1098 GVVTVTVAEGDEVKAGDAVAITEAMKMEATITASVDGKITERVVVPAATKVEGGDLIVVVS 1157
 Db 1081 GVVTVTVAEGDEVKAGDAVAITEAMKMEATITASVEGKIDRVVVVPAATKVEGGDLIVVVS 1140
 RESULT 3
 AAB01436
 ID AAB01436 standard; Protein; 1141 AA.
 AC AAB01436;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE Pyruvate carboxylase of C. glutamicum.

XX	Pyruvate carboxylase; expression: amino acid biosynthesis; lysine;
KW	glutamic acid; oxaloacetate; fermentation; biosynthesis.
XX	Corynebacterium glutamicum.
XX	WO200039305-A1.
XX	06-JUL-2000.
XX	23-DEC-1998; 98WO-US27301.
XX	23-DEC-1998; 98WO-US27301.
XX	(SINS/) SINSKEY A J.
PA	(LESS/) LESSARD P A.
PA	(WILL/) WILLIS L B.
XX	Sinskey AJ, Lessard PA, Willis LB;
XX	WPI: 2000-465746/40.
XX	DR N-PSDB; AAA47533.
XX	Novel polynucleotides encoding Corynebacterium glutamicum pyruvate
PT	carboxylase useful for industrial fermentation processes comprises a
PT	specific nucleotide sequence
XX	Claim 3; Fig 1; 51pp; English.
XX	The pyruvate carboxylase of Corynebacterium glutamicum can be used
CC	for producing amino acids, preferably lysine and glutamic acid in
CC	industrial fermentations and for replenishing oxaloacetate consumed
CC	for biosynthesis during growth. By incorporating the pyruvate
CC	carboxylase gene in expression vectors levels of expression can be
CC	2 - 20 fold higher than in Corynebacterium glutamicum.
XX	Sequence 1141 AA;
SQ	Query Match 98.3%; Score 5764; DB 21; Length 1141;
	Best Local Similarity 99.4%; Pred. No. 0;
	Matches 1134; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY	17 LVSHHTSTLPAFKKILVANGETAVAFRAALETGAAIVAIYPREDRGSFHRSPASEAV 76
Db	1 MVSTHTSTLPAFKKILVANGETAVAFRAALETGAAIVAIYPREDRGSFHRSPASEAV 60
QY	77 RIGTEGSPVKAYLDIDELIGAAKKVKADAIYPGYGLSENAQLARECAENGITFTGPTPE 136
Db	61 RIGTEGSPVKAYLDIDELIGAAKKVKADAIYPGYGLSENAQLARECAENGITFTGPTPE 120
QY	137 VLDLTGDKSRVTAARKAGLPVLAESTPSKNDDIVKSAEGQYPIFFKAVAGGGGRMR 196
Db	121 VLDLTGDKSRVTAARKAGLPVLAESTPSKNDDIVKSAEGQYPIFFKAVAGGGGRMR 180
QY	197 FVSSPDELRLKLTASREAAAFDGSVYVERAVINPQHIEVOILGDRTGEVVHLYERDC 256
Db	181 FVASPDELRLKLTASREAAAFDGSVYVERAVINPQHIEVOILGHTGEVVHLYERDC 240
QY	257 SLQRHQKVVETIAPAHLDPQLDRICADAVKFCRSIGYAGTVEFLVDEKGNHVFIEM 316
Db	241 SLQRHQKVVETIAPAHLDPQLDRICADAVKFCRSIGYAGTVEFLVDEKGNHVFIEM 300
QY	317 NPRIQVETVTEEVTEVDLVKAQMRLAAGATLKEGLGTQDKIKTHGAALQCRTTDDPNN 376
Db	301 NPRIQVETVTEEVTEVDLVKAQMRLAAGATLKEGLGTQDKIKTHGAALQCRTTDDPNN 360
QY	377 GFRPDTGITAYRSPGGAGVRLDGAALGGGEITAHFDSMLVKMTCRGSDFETAVARAQRA 436
Db	361 GFRPDTGITAYRSPGGAGVRLDGAALGGGEITAHFDSMLVKMTCRGSDFETAVARAQRA 420
QY	437 LAEFTVSGVATNIGFLRALNREEDFTSKRIATQFIGDHPHLQAPPADDEQGRILDYAD 496
Db	421 LAEFTVSGVATNIGFLRALNREEDFTSKRIATQFIGDHPHLQAPPADDEQGRILDYAD 480

PR 03-AUG-2000; 2000JP-0280988.
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX WPI; 2001-376931/40.
 DR N-PSDB; AAH65730.
 XX Novel polynucleotides derived from Corynebacterium bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analysing
 PT expression profile or pattern of a gene and identifying homologous gene
 PT
 XX
 PS Claim 17; SEQ ID NO: 4265; 246pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of corynebacterium, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from Corynebacterium, and identifying a homologue of a gene derived
 CC from corynebacterium. Corynebacterium bacteria are useful for producing
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a protein described
 CC in the exemplification of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.
 XX
 SQ Sequence 1140 AA;
 Query Match 98.2%; Score 5759; DB 22; Length 1140;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1133; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 18 VSTHTSSLPAPKTLIVANRGEIAVRAFALETAATVAIYPREDRGSFHRSPASEAVR 77
 Db :|||||
 QY 1 MSTHTSSLPAPKTLIVANRGEIAVRAFALETAATVAIYPREDRGSFHRSPASEAVR 60
 QY 78 IGTEGSPKAYLDDIETIGAAKKVADAIYGYGFLSNAQLARECAENGITFPGTPEV 137
 Db :|||||
 QY 61 IGTEGSPKAYLDDIETIGAAKKVADAIYGYGFLSNAQLARECAENGITFPGTPEV 120
 QY 138 LDLTGDKSRAYTAARKAGLPVLAESTPSKNIDDIKSAEGQTYPIFVKAVAGGGGRMRF 197
 Db :|||||
 QY 121 LDLTGDKSRAYTAARKAGLPVLAESTPSKNIDDIKSAEGQTYPIFVKAVAGGGGRMRF 180
 QY 198 VSSPDELRLKATEASREAEAFGDSGVYVERAVINPQHEIYQILGDRGTGVVHLYERDCS 257
 Db :|||||
 QY 191 VASPDDELRLKATEASREAEAFGDSGVYVERAVINPQHEIYQILGDRGTGVVHLYERDCS 240
 QY 258 LQRRHQKVEIAPAGHLDPELRDRIKADAVKFCRSIGYOGAGTVEFLYDEKGNHVFIEMN 317
 Db :|||||
 QY 241 LQRRHQKVEIAPAGHLDPELRDRIKADAVKFCRSIGYOGAGTVEFLYDEKGNHVFIEMN 300
 QY 318 PRIQVEHTVTEVTEVDLVKQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNNG 377
 Db :|||||
 QY 301 PRIQVEHTVTEVTEVDLVKQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNNG 360
 QY 378 FRPDGTITAYRSPGAGVRLDGAQLGGEITAHFDSMLVMTKRGSDFTAVARAQAL 437
 Db :|||||
 QY 361 FRPDGTITAYRSPGAGVRLDGAQLGGEITAHFDSMLVMTKRGSDFTAVARAQAL 420
 QY 438 AEFTVSGVATNIGFALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYADV 497
 Db :|||||
 QY 421 AEFTVSGVATNIGFALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYADV 480
 QY 498 TVNPKHGVKPDVAAPIDKLPNIDPLPRGSRDRKLGPAFAFARDLREQDALAVTDTT 557
 Db :|||||
 QY 481 TVNPKHGVKPDVAAPIDKLPNIDPLPRGSRDRKLGPAFAFARDLREQDALAVTDTT 540

QY 558 FRDAHOSLLATVRVSFALKPAAEAVALKTPELLSSVEAWGATYDVAMRFLFEDPDWRDLE 617
 Db :|||||
 QY 541 FRDAHOSLLATVRVSFALKPAAEAVALKTPELLSSVEAWGATYDVAMRFLFEDPDWRDLE 600
 QY 618 LREAMPNNVNIOMLLRGRNTVGYTPYSDSVCRAFVKEAASSGVDFIFRIFDALNDVSOMRPA 677
 Db :|||||
 QY 601 LREAMPNNVNIOMLLRGRNTVGYTPYSDSVCRAFVKEAASSGVDFIFRIFDALNDVSOMRPA 660
 QY 678 IDAVLETNTAVAEVAMAYSGDLSNDNEKLYTIDYLYKMAEEIVKSGAHILAIKDMAGLLR 737
 Db :|||||
 QY 661 IDAVLETNTAVAEVAMAYSGDLSNDNEKLYTIDYLYKMAEEIVKSGAHILAIKDMAGLLR 720
 QY 738 PAAVTKLYTALRREFDLPVHVHTHTAGGOLATYFAAAQAGADAVDVGASAPLSGTTSQPS 797
 Db :|||||
 QY 721 PAAVTKLYTALRREFDLPVHVHTHTAGGOLATYFAAAQAGADAVDVGASAPLSGTTSQPS 780
 QY 798 LSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGVLYLPESGTPGTGRVYRHEIPGGQL 857
 Db :|||||
 QY 781 LSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGVLYLPESGTPGTGRVYRHEIPGGQL 840
 QY 858 SNLRAQATAGLADRFELIEDNYAANEMLGPRTKVTPTSSKVVGDALHLVAGVDPADF 917
 Db :|||||
 QY 841 SNLRAQATAGLADRFELIEDNYAANEMLGPRTKVTPTSSKVVGDALHLVAGVDPADF 900
 QY 918 AADPKYDIPDSVIAFLRGLGNPPGWPPEPLTRALEGRSGKAPLTVPEPEOAHLLDA 977
 Db :|||||
 QY 901 AADPKYDIPDSVIAFLRGLGNPPGWPPEPLTRALEGRSGKAPLTVPEPEOAHLLDA 960
 QY 978 DDSKERRNSLNLLFPKPTTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLRLPDVRTP 1037
 Db :|||||
 QY 961 DDSKERRNSLNLLFPKPTTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLRLPDVRTP 1020
 QY 1038 LLVRLDAISEPDDKGMNVNANVNGQIRPMRVDRSVESVTATAEKADSSNKGHVAAPPA 1097
 Db :|||||
 QY 1021 LLVRLDAISEPDDKGMNVNANVNGQIRPMRVDRSVESVTATAEKADSSNKGHVAAPPA 1080
 QY 1098 GVVTVTVAGDEVKAGDAVAIIEMKMEATITASVDGKIERYVVPAAATKVEGGDLIVVVS 1157
 Db :|||||
 QY 1081 GVVTVTVAGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAAATKVEGGDLIVVVS 1140
 RESULT 5
 AAB67129
 ID AAB67129 standard; Protein; 1140 AA.
 XX
 AC AAB67129;
 XX
 DT 12-APR-2001 (first entry)
 XX
 DE Corynebacterium glutamicum pyruvate carboxylase.
 XX
 KW Pyruvate carboxylase; anaplerotic pathway; industrial fermentation;
 KW oxaloacetate.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN US6171833-B1.
 XX
 PD 09-JAN-2001.
 XX
 PF 23-DEC-1998; 98US-0220081.
 XX
 PR 23-DEC-1998; 98US-0220081.
 XX
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX
 PI Sinskey AJ, Lessard PA, Willis LB;
 XX
 DR WPI; 2001-122330/13.
 XX
 DR N-PSDB; AAF32165.
 XX
 PT Novel nucleic acid encoding pyruvate carboxylase from Corynebacterium
 PT glutamicum, for replenishing oxaloacetate consumed during lysine and

PT	glutamic acid production in industrial fermentations -	
XX	Claim 1; Column 31-36; 29pp; English.	
XX	The present invention provides the protein and coding sequences of the	
CC	Corynebacterium glutamicum pyruvate carboxylase protein. This is an	
CC	enzyme in the anaplerotic pathway. It can be used in the replenishment of	
CC	oxaloacetate consumed during lysine and glutamic acid production in	
CC	industrial fermentation.	
XX		
SQ	Sequence 1140 AA;	
Query Match	98.2%; Score 5759; DB 22; Length 1140;	
Best Local Similarity	99.4%; Pred. No. 0;	
Matches 1133; Conservative	5; Mismatches 2; Indels 0; Gaps 0;	
QY	18 VSTHTSSTLPAPFKKILVANRGRIAVRAFAALETGAATVAIYPREDRSGFHSFASAVR 77	
DB	1 MSTHTSSILPAPFKKILVANRGRIAVRAFAALETGAATVAIYPREDRSGFHSFASAVR 60	
QY	78 IGTGSPVKAYLDIDEIIGAARKKADAIYGYGFLSENAQLARECAENGITFIGPTPEV 137	
DB	61 IGTGSPVKAYLDIDEIIGAARKKADAIYGYGFLSENAQLARECAENGITFIGPTPEV 120	
QY	138 LDLTGDKSRAYTAARKAGLPVLAESTPSKNIDDIIVKSAEGQYPIFVKAVAGGGGMR 197	
DB	121 LDLTGDKSRAYTAARKAGLPVLAESTPSKNIDDIIVKSAEGQYPIFVKAVAGGGGMR 180	
QY	198 VSSDELKRLATEASREAAFGDGVVYERAVINPOHIEVQILGDRGVEVHLYERDCS 257	
DB	181 VASDELKRLATEASREAAFGDGVVYERAVINPOHIEVQILGDRGVEVHLYERDCS 240	
QY	258 LQRRHQKVEIAPQAHLDELDRICADAVFCRSIGYGAGTVEFLVDEKGNHVFIEWN 317	
DB	241 LQRRHQKVEIAPQAHLDELDRICADAVFCRSIGYGAGTVEFLVDEKGNHVFIEWN 300	
QY	318 PRIQVEHVTVEVTVLKVAKMRLAAGATKELGLTQKIKTHGAALQCRITTEDPNN 377	
DB	301 PRIQVEHVTVEVTVLKVAKMRLAAGATKELGLTQKIKTHGAALQCRITTEDPNN 360	
QY	378 FRPDGTITAYRSPGAGVRDGAAGLGEITAHEDSMLVKMTCRGSDFETAVARAQAL 437	
DB	361 FRPDGTITAYRSPGAGVRDGAAGLGEITAHEDSMLVKMTCRGSDFETAVARAQAL 420	
QY	438 AEFTVSGVATNIGFALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYAD 497	
DB	421 AEFTVSGVATNIGFALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYAD 480	
QY	498 TVNKPVGVRPKDVAAPIDKLPNIKDLPLGRSRRDLKOLGPAAPARDLREQDALAVDTT 557	
DB	481 TVNKPVGVRPKDVAAPIDKLPNIKDLPLGRSRRDLKOLGPAAPARDLREQDALAVDTT 540	
QY	558 FRDHAQSLLATVRFSFALKPAEAAVAKLTPELLSVEAMGGATYDVAMRFLFEDPMDRLDE 617	
DB	541 FRDHAQSLLATVRFSFALKPAEAAVAKLTPELLSVEAMGGATYDVAMRFLFEDPMDRLDE 600	
QY	618 LREAMPNVIOMLLGRNTGYTPYPSVCRAFVKEAASSGVDFIPRIFDALNDVSQMPA 677	
DB	601 LREAMPNVIOMLLGRNTGYTPYPSVCRAFVKEAASSGVDFIPRIFDALNDVSQMPA 660	
QY	678 IDAVLETNTVAEAMAYSGDLSOPNEKLYTLDYLYKMAEIVKSGAHILAIDKMAGLLR 737	
DB	661 IDAVLETNTVAEAMAYSGDLSOPNEKLYTLDYLYKMAEIVKSGAHILAIDKMAGLLR 720	
QY	738 PAAVTKLVTALRREFDLPHVHTHTDAGQIATYFAAAQAGADAVDGSAPLSGTTSPQS 797	
DB	721 PAAVTKLVTALRREFDLPHVHTHTDAGQIATYFAAAQAGADAVDGSAPLSGTTSPQS 780	
QY	798 LSAIVAAFAHTRDRTGLSLEAVSDLEPYWEAVRGILYLPFESGTPGTRVYRHEIPGQOL 857	
DB	781 LSAIVAAFAHTRDRTGLSLEAVSDLEPYWEAVRGILYLPFESGTPGTRVYRHEIPGQOL 840	
QY	858 SNLRAQATAGLADRFELIEDNYAAVNEMLGRPTKVTPTSSKVVGDALHLVAGVDPADF 917	
DB	841 SNLRAQATAGLADRFELIEDNYAAVNEMLGRPTKVTPTSSKVVGDALHLVAGVDPADF 900	
QY	918 RADPOKYDIPDSVIAFLRGELGNPPGGWPEPLRTALSGRSGKAPLTVPEEQAHLLDA 977	
DB	901 RADPOKYDIPDSVIAFLRGELGNPPGGWPEPLRTALSGRSGKAPLTVPEEQAHLLDA 960	
QY	978 DDSKERRNSLNRLLEFPKTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTP 1037	
DB	961 DDSKERRNSLNRLLEFPKTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTP 1020	
QY	1038 LLVRLDAISEPDDKGMNVVANVNGQIRPMRVDRSVESVTATAEKADSSNKGHVAAPFA 1097	
DB	1021 LLVRLDAISEPDDKGMNVVANVNGQIRPMRVDRSVESVTATAEKADSSNKGHVAAPFA 1080	
QY	1098 GVVTVTVAGDEVKAGDAVAIIEAMKMEATITASVDGKIERYVPAATKVEGGDLIVVVS 1157	
DB	1081 GVVTVTVAGDEVKAGDAVAIIEAMKMEATITASVDGKIERYVPAATKVEGGDLIVVVS 1140	
RESULT 6		
AAE25601		
ID	AAE25601 standard; Protein; 1140 AA.	
XX	AAE25601;	
XX	04-NOV-2002 (first entry)	
XX	Corynebacterium glutamicum pyruvate carboxylase protein.	
XX	Pyruvate carboxylase; anaplerotic enzyme; industrial fermentation;	
XX	oxaloacetate; growth; enzyme.	
XX	Corynebacterium glutamicum.	
XX	Key Location/Qualifiers	
FT	Misc-difference 1 /note= "Encoded by GTG"	
XX	US6403351-B1.	
XX	11-JUN-2002.	
XX	03-OCT-2000; 2000US-0677575.	
XX	23-DEC-1998; 98US-0220081.	
XX	(ARCH) ARCHER-DANIELS MIDLAND CO.	
XX	Sinskey AJ, Lessard PA, Willis LB;	
XX	WPI; 2002-536037/57.	
XX	N-PSDB; AAD42046.	
XX	Novel pyruvate carboxylase polypeptide, useful for replenishing	
XX	oxaloacetate consumed for biosynthesis during growth, or lysine and	
XX	glutamic acid production in industrial fermentation -	
XX	Claim 1; Column 29-36; 28pp; English.	
XX	The present invention relates to novel pyruvate carboxylase proteins and	
XX	polynucleotides encoding such proteins. Sequences of the invention are	
XX	important anaplerotic enzymes for replenishing oxaloacetate consumed for	
XX	biosynthesis during growth, or lysine and glutamic acid production in	
XX	industrial fermentation. The present sequence is C. glutamicum pyruvate	
XX	carboxylase protein.	
SQ	Sequence 1140 AA;	
Query Match	98.2%; Score 5759; DB 23; Length 1140;	
Best Local Similarity	99.4%; Pred. No. 0;	
Matches 1133; Conservative	5; Mismatches 2; Indels 0; Gaps 0;	

QY 18 VSTHTSSTLPAPKKILVANRGEIIVAFRAALETGAATVAIYPREDRGSPHRSFASAVR 77
Db 1 MSHTSSTLPAPKKILVANRGEIIVAFRAALETGAATVAIYPREDRGSPHRSFASAVR 60
QY 78 IGTEGSPVKAYLDIDEIIGAARKKADAIYPGYFLSENAQLARECAENGITFTGPTPEV 137
Db 61 IGTEGSPVKAYLDIDEIIGAARKKADAIYPGYFLSENAQLARECAENGITFTGPTPEV 120
QY 138 LDLTGDKSRVATAAKKAGLPVLAESTPSKNIDDIIVKSAEGOTYPIFYKAVAGGGGRMRF 197
Db 121 LDLTGDKSRVATAAKKAGLPVLAESTPSKNIDDIIVKSAEGOTYPIFYKAVAGGGGRMRF 180
QY 198 VSSPDELKRLATEASRAEAFGDSYVVERAVINPOHIEVQIILGDTGEVHLYERDCS 257
Db 181 VASPEDELKRLATEASRAEAFGDSYVVERAVINPOHIEVQIILGDTGEVHLYERDCS 240
QY 258 LQRHOKVETAPAHLDPELRDRIKADAVKFCRSIGYOGAGTVEEVLVDEKGNHVFTEMN 317
Db 241 LQRHOKVETAPAHLDPELRDRIKADAVKFCRSIGYOGAGTVEEVLVDEKGNHVFTEMN 300
QY 318 PRIQVHTVTEEVTEVDLVKAQMLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNN 377
Db 301 PRIQVHTVTEEVTEVDLVKAQMLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNN 360
QY 378 FRPDGTGITAVRSPGGAGVRLDGAALGGGSEITAHFDSMLVKMTCRGSDFFETAVARAQAL 437
Db 361 FRPDGTGITAVRSPGGAGVRLDGAALGGGSEITAHFDSMLVKMTCRGSDFFETAVARAQAL 420
QY 438 AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIQDHPHLLQAPPADDEOGRILLYLADV 497
Db 421 AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIQDHPHLLQAPPADDEOGRILLYLADV 480
QY 498 TVNKPQVPRKDVAAPIKDKLPNTKIDPLPRGSRDLKQLGPAAPFARDLRQDALAVTDIT 557
Db 481 TVNKPQVPRKDVAAPIKDKLPNTKIDPLPRGSRDLKQLGPAAPFARDLRQDALAVTDIT 540
QY 558 FRDAHOSLLATRVRSFALKPAEAAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWRDLDE 617
Db 541 FRDAHOSLLATRVRSFALKPAEAAVAKLTPELLSVEAWGGATYDVAMRFLFEDPWRDLDE 600
QY 618 LREAMPNVIQMLLRGNTVGYTYPDSCVAFVKEAASSGVDFIRFDALNDVQMRPA 677
Db 601 LREAMPNVIQMLLRGNTVGYTYPDSCVAFVKEAASSGVDFIRFDALNDVQMRPA 660
QY 678 IDAVLENTAVAVAMAYSGDSDPNEKLYTLDYILKMAEIVKSAHILAIKDMAGLLR 737
Db 661 IDAVLENTAVAVAMAYSGDSDPNEKLYTLDYILKMAEIVKSAHILAIKDMAGLLR 720
QY 738 PAAVTKLVTLALRREFDLPVHVHTDAGGOLATYFAAQAQADAVDAGASAPLSGTTSPQS 797
Db 721 PAAVTKLVTLALRREFDLPVHVHTDAGGOLATYFAAQAQADAVDAGASAPLSGTTSPQS 780
QY 798 LSAIVAFAHTRDRTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 857
Db 781 LSAIVAFAHTRDRTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 840
QY 858 SNLRAQATGLADRELELDNAAVNEMLGRPTKVTGPSKVVGDIALHLVAGVDPADP 917
Db 841 SNLRAQATGLADRELELDNAAVNEMLGRPTKVTGPSKVVGDIALHLVAGVDPADP 900
QY 918 AADPQKYDIPDSVIAFLRGELGNPPGWPPELURTRALEGRSEKAPLTVEPEEQAHLD 977
Db 901 AADPQKYDIPDSVIAFLRGELGNPPGWPPELURTRALEGRSEKAPLTVEPEEQAHLD 960
QY 978 DSKERNRSLNLLPKPTEEFLEHRRRFGNTSALDDREFFYGLVREGTTLRLPVRTP 1037
Db 961 DSKERNRSLNLLPKPTEEFLEHRRRFGNTSALDDREFFYGLVREGTTLRLPVRTP 1020
QY 1038 LLVRLDAISEPDDKGMNRVAVNVNGQIRPMVRDRSVESVTATAEKADSSNKGHVAAPFA 1097
Db 1021 LLVRLDAISEPDDKGMNRVAVNVNGQIRPMVRDRSVESVTATAEKADSSNKGHVAAPFA 1080
QY 1098 GVVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVPAATKVEGGDLIVVVS 1157

Db 1081 GVVTVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVPAATKVEGGDLIVVVS 1140
RESULT 7
AAU98053
ID AAU98053 standard; Protein; 1140 AA.
XX AAU98053;
AC AAU98053;
DT 27-AUG-2002 (first entry)
XX Corynebacterium wild-type feedback-resistant pyruvate carboxylase enzyme.
DE Feedback-resistant; pyruvate carboxylase; enzyme;
XX aspartic acid feedback inhibition resistant.
KW Corynebacterium glutamicum.
XX WO200231158-A2.
XX 18-APR-2002.
XX 12-OCT-2001; 2001WO-US31893.
XX 13-OCT-2000; 2000US-239913P.
XX (ARCH) ARCHER-DANIELS MIDLAND CO.
XX Hanke PD;
XX WPI; 2002-463267/49.
XX Novel mutated, feedback resistant pyruvate carboxylase enzyme
PT polypeptide, useful for producing amino acids e.g. L-lysine,
PT L-threonine, L-glycine, L-glutamic acid, L-proline and L-methionine and
PT L-isoleucine.
XX Disclosure; Fig 2; 42pp; English.
XX The present invention relates to a new mutated, feedback-resistant
XX pyruvate carboxylase enzyme. The invention is useful for producing an
XX amino acid (e.g. L-Lys, L-Thr, L-Met, L-Ile, L-Glu, L-Arg and L-Pro),
XX by culturing a host cell in a suitable media and separating the amino
XX acid from the medium. The vector of the invention is useful for
XX replacement of a wild-type pyruvate carboxylase gene, with a feedback
XX resistant pyruvate carboxylase gene, in a Corynebacterium glutamicum, by
XX replacing a genomic copy of the wild-type pyruvate carboxylase gene with
XX a selectable marker gene through homologous recombination to form a first
XX recombination strain, and replacing the selectable marker gene in the
XX first recombination strain, with feedback resistant pyruvate carboxylase
XX gene through homologous recombination to form a second recombinant
XX strain, where the homologous recombination in the above steps, occurs
XX between the host cell and the vector. The feedback-resistant pyruvate
XX carboxylase enzyme is resistant to feedback inhibition from aspartic
XX acid. The present amino acid sequence represents the wild-type
XX feedback-resistant pyruvate carboxylase enzyme of the invention.
XX Sequence 1140 AA;

Query Match 98.2%; Score 5759; DB 23; Length 1140;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1133; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 18 VSTHTSSTLPAPKKILVANRGEIIVAFRAALETGAATVAIYPREDRGSPHRSFASAVR 77
Db 1 MSHTSSTLPAPKKILVANRGEIIVAFRAALETGAATVAIYPREDRGSPHRSFASAVR 60
QY 78 IGTEGSPVKAYLDIDEIIGAARKKADAIYPGYFLSENAQLARECAENGITFTGPTPEV 137
Db 61 IGTEGSPVKAYLDIDEIIGAARKKADAIYPGYFLSENAQLARECAENGITFTGPTPEV 120
QY 138 LDLTGDKSRVATAAKKAGLPVLAESTPSKNIDDIIVKSAEGOTYPIFYKAVAGGGGRMRF 197

Db 121 LDLTGDKSRVTAAKKAGLVLAESTPSKNIDELVKSAGQTPYIFVKAVAGGGRGMRF 180
 QY 198 VSSPDELRLKLTASREAEAFSGSVYVERAVINPOHIEVQILGORTGEVHLYERDCS 257
 Db 181 VASPELRLKLTASREAEAFSGSVYVERAVINPOHIEVQILGORTGEVHLYERDCS 240
 QY 258 LORRHOKVVEIAPAHLDPELRDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFEMN 317
 Db 241 LORRHOKVVEIAPAHLDPELRDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFEMN 300
 QY 318 PRIQVEHTVTEVTEVDLVKAQMLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG 377
 Db 301 PRIQVEHTVTEVTEVDLVKAQMLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG 360
 QY 378 FREDTGITITAYRSPGGAGVRLDCAAGLGGGTTAHFDSMLVKMTCRSGDFETAVARAQAL 437
 Db 361 FREDTGITITAYRSPGGAGVRLDCAAGLGGGTTAHFDSMLVKMTCRSGDFETAVARAQAL 420
 QY 438 AETVSGVATNIGFLRALREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYADV 497
 Db 421 AETVSGVATNIGFLRALREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYADV 480
 QY 498 TVNKPGRVPRKDVAAPTDKLPNTKDLPLPRGSRDLKQLGPAFAFADRLRQDALAVTDYT 557
 Db 481 TVNKPGRVPRKDVAAPTDKLPNTKDLPLPRGSRDLKQLGPAFAFADRLRQDALAVTDYT 540
 QY 558 FRDHQSLLATRVRSFALKPAEAVAKLTPELLSVEAWGATYDVAMRFLFEDPWRDLDE 617
 Db 541 FRDHQSLLATRVRSFALKPAEAVAKLTPELLSVEAWGATYDVAMRFLFEDPWRDLDE 600
 QY 618 LREAMPNVQMLLRGNITVGYTPYDPSVCRAVKEAASGVDFIRIFDALNDVQMRPA 677
 Db 601 LREAMPNVQMLLRGNITVGYTPYDPSVCRAVKEAASGVDFIRIFDALNDVQMRPA 660
 QY 678 IDAVLENTAVAEVAMAYSGDLSDPNEKLYTLDYILKMAEIVKSAHILAIKDMAGLLR 737
 Db 661 IDAVLENTAVAEVAMAYSGDLSDPNEKLYTLDYILKMAEIVKSAHILAIKDMAGLLR 720
 QY 738 PAATVKTVALRREFDLPVHVHTHDPAGGLATYFAAAGADAVDGSAPLSGTTSQPS 797
 Db 721 PAATVKTVALRREFDLPVHVHTHDPAGGLATYFAAAGADAVDGSAPLSGTTSQPS 780
 QY 798 LSAIVAFAHTRDTGLSEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 857
 Db 781 LSAIVAFAHTRDTGLSEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 840
 QY 858 SNLRAQATAGLADREFELIEDNYAAVNEMLGRPTKVTPSSKVVGDALHLVAGVDPADF 917
 Db 841 SNLRAQATAGLADREFELIEDNYAAVNEMLGRPTKVTPSSKVVGDALHLVAGVDPADF 900
 QY 918 AADPKYDIPDSVIAFLRGELGNPPGWPPEPLTRALEGRSEKAPLTVPEEQAHLDA 977
 Db 901 AADPKYDIPDSVIAFLRGELGNPPGWPPEPLTRALEGRSEKAPLTVPEEQAHLDA 960
 QY 978 DSKERNLSNRLFPKPEEFLHRRRFGNTSALDDREFFYGLVGGRETLRLPDRVTP 1037
 Db 961 DSKERNLSNRLFPKPEEFLHRRRFGNTSALDDREFFYGLVGGRETLRLPDRVTP 1020
 QY 1038 LVLRLDAISEPDKGMNRNVVAVNGQIRPMRVDRDSVESVTATAEKADSSNKGHVAAPPA 1097
 Db 1021 LVLRLDAISEPDKGMNRNVVAVNGQIRPMRVDRDSVESVTATAEKADSSNKGHVAAPPA 1080
 QY 1098 GVVTVTVAEGDEVKAGDAVAIIEMKMEATITASVDGKITERVVVPAATKVEGGDLIVVVS 1157
 Db 1081 GVVTVTVAEGDEVKAGDAVAIIEMKMEATITASVDGKITERVVVPAATKVEGGDLIVVVS 1140

RESULT 8
 AAW93971
 ID AAW93971 standard; Protein; 1140 AA.
 XX
 AC AAW93971;

XX 30-JUN-1999 (first entry)
 DT C. glutamicum pyruvate carboxylase protein.
 DE Pyruvate carboxylase; amino acid production; lysine production;
 XX threonine production; homoserine production; glutamate production;
 KW arginine production; feed additive; condiment; pharmaceutical;
 KW fine chemical; ss.
 XX Corynebacterium glutamicum.
 OS DE19831609-A1.
 XX PN 15-APR-1999.
 XX PF 14-JUL-1998; 98DE-1031609.
 XX PR 04-OCT-1997; 97DE-1043894.
 XX PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
 XX PI Eikmanns B, Peters-Wendisch P, Sahm H;
 XX WP1: 1999-245521/21.
 DR N-PSDB; AAX24102.
 XX Increasing microbial production of specific amino acids by
 PT increasing activity or expression of pyruvate carboxylase
 XX Claim 15; Page 11-15; 18pp; German.
 XX This invention describes the isolation of a pyruvate carboxylase
 CC from Corynebacterium glutamicum which is used in a novel method for
 CC production of lysine, threonine, homoserine, glutamate and/or arginine,
 CC variously useful as feed additives, condiments, pharmaceuticals and
 CC intermediates for fine chemicals. Increasing pyruvate carboxylase
 CC activity increases the yield of microbial production of amino acids
 CC of the aspartate and/or glutamate families, e.g. about 50% more lysine,
 CC 40% more threonine and 150% more homoserine are secreted into the
 CC culture medium.
 XX Sequence 1140 AA;
 SQ Query Match 98.1%; Score 5753; DB 20; Length 1140;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 1132; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
 QY 18 VSTHTSSTLPAPFKKILVANRGEITAVRAALETGAATVAIYPRDRGSHRSFASAYR 77
 Db 1 MSTHTSSTLPAPFKKILVANRGEITAVRAALETGAATVAIYPRDRGSHRSFASAYR 60
 QY 78 ICTEGSPVKAYLDIDEIIGAANKVADAIYPGYGFLSENAQLARECAENGITFIGPTPEV 137
 Db 61 ICTEGSPVKAYLDIDEIIGAANKVADAIYPGYGFLSENAQLARECAENGITFIGPTPEV 120
 QY 138 LDLTGDKSRVTAAKKAGLVLAESTPSKNIDDIKSAEGQTPYIFVKAVAGGGRGMRF 197
 Db 121 LDLTGDKSRVTAAKKAGLVLAESTPSKNIDDIKSAEGQTPYIFVKAVAGGGRGMRF 180
 QY 198 VSSPDELRLKLTASREAEAFSGSVYVERAVINPOHIEVQILGORTGEVHLYERDCS 257
 Db 181 VASPELRLKLTASREAEAFSGSVYVERAVINPOHIEVQILGORTGEVHLYERDCS 240
 QY 258 LORRHOKVVEIAPAHLDPELRDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFEMN 317
 Db 241 LORRHOKVVEIAPAHLDPELRDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFEMN 300
 QY 318 PRIQVEHTVTEVTEVDLVKAQMLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG 377
 Db 301 PRIQVEHTVTEVTEVDLVKAQMLAAGATLKELGLTQDKIKTHGAALQCRITTEDPNNG 360
 QY 378 FREDTGITITAYRSPGGAGVRLDCAAGLGGGTTAHFDSMLVKMTCRSGDFETAVARAQAL 437

20-JUN-2001.
18-DEC-2000; 2000EP-0127688.
16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
(KYOW) KYOWA HAKKO KOGYO KK

Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene

Claim 43; Page -: 246pp + Sequence Listing; English.

The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium *Corynebacterium glutamicum*. These sequences are useful for identifying the mutation point of a gene derived from a mutant of *coryneform bacterium*, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from *Coryneform bacterium*, and identifying a homologue of a gene derived from *coryneform bacterium*. *Coryneform bacteria* are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a mutant protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.

Sequence 1140 AA:

Query Match

Best Local Similarity 99.3%; Pred No. 0;

Best local similarity 99.3%, Fied. NO: 0;
Matches 1132; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 18 VSTHTSSITLPAFKKILVANGETAVRAFAALETGAATVAIYPRDRGSGTHRSFASEAVR 77
: |||||
Db 1 MSTHTSSITLPAFKKILVANGETAVRAFAAIETGAATVAIYDPRGSGTHRSFASEAVR 60

QY 78 IGTEGSPVKAYLDIDEIIGAAKKVKADATYPGYGELSENQALRCAENGITFIGTPEV 137
|||||
Db 61 IGTEGSPVKAYLDIDEIIGAAKKVKADATYPGYGELSENQALRCAENGITFIGTPEV 120
|||||

QY 138 LDLTGDKSRVTAACKAGLPVLAESTPSKNIDDIVKSAEGOTYPPIFVKAVAGGGGGRGMRF 197

Db 121 LDLTGDKSRVTAAKKAGLPVLAESTPSKNIDEIVKSAEGQTYPIFVKAVAGGGGRGMRF 180

QY 198 VSSPDELKRLATEASREAEAFGDGVSYYVERAVINPQHIEVQILGDRGTGEVHLYERDCS 257

Db 181 VASPELRLKATEASREAEAAFGDGA VYVERAVINPQHIEVQILGDHTGEV VHL YERDCS 240

QY 258 LQRRHQVWEIAPAQHLDPQLDRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFIEMN 317

DD 241 LQRRHQVVEIAPFAQHLDPELRDRICADAVKFCRSTGYQGAGTVEFLVDERGNHVFTEMN 300

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1. The first step is to identify the problem or question that needs to be addressed. This involves understanding the context and the specific requirements of the task.

2. Next, it is important to gather relevant information and data. This can be done through research, consultation with experts, or by analyzing existing resources.

3. Once the information is gathered, the next step is to develop a plan or strategy. This involves breaking down the problem into smaller, manageable parts and determining the best approach to solve each part.

4. The fourth step is to implement the plan. This involves putting the strategy into action and monitoring progress along the way.

5. Finally, it is essential to evaluate the results and make adjustments as needed. This involves comparing the actual outcomes with the expected results and identifying any areas for improvement.

6. The process of problem-solving is often iterative, meaning that it may involve going back and forth between different steps as more information is gained or as the situation evolves.

7. It is also important to communicate effectively throughout the process. This involves sharing information with others who may be involved in the project and seeking feedback to ensure that everyone is on the same page.

8. Finally, it is crucial to document the process and the results. This helps to ensure that the information is preserved and can be used as a reference for future projects.

9. The overall goal of the problem-solving process is to find a solution that is effective, efficient, and sustainable. This requires a combination of critical thinking, creativity, and collaboration.

10. By following these steps, individuals and teams can approach problems with confidence and increase their chances of finding a successful solution.

RESULT 9
AAG93249
ID AAG93249 standard; Protein; 1140 AA.
XX
AC AAG93249;
XX
DT 26-SEP-2001 (first entry)

C glutamicum protein fragment mutant p458s.

Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; mutant; mutein.

Corynebacterium glutamicum.

Synthetic.

Key	Location/Qualifiers
vi-3:55	150

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# Difference 450
#note= "wild-type pr

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EP1108790-A2.

Db 421 AEFVSVATNIGLRLALLREEDFTSKRIATGFIADHSHLLQAPPADDEQGRILDIADY 480
 QY 498 TVNKPGRVPRKVAAPIDKLPNIKDLPLPRGSRDLKQLGPAFAFARDLRQDALAVTDIT 557
 Db 481 TVNKPGRVPRKVAAPIDKLPNIKDLPLPRGSRDLKQLGPAFAFARDLRQDALAVTDIT 540
 QY 558 FRAHQSLLATRVRSFALKAFAAVALKIPPELLSVEAGGATYDVAMRFLFEDPWRDLDE 617
 Db 541 FRAHQSLLATRVRSFALKAFAAVALKIPPELLSVEAGGATYDVAMRFLFEDPWRDLDE 600
 QY 618 LREAMPNVIOMLLRGNTVGYTPYDPSVCRAFPVKEAASGVDIFRIFDALNDVDSQMRPA 677
 Db 601 LREAMPNVIOMLLRGNTVGYTPYDPSVCRAFPVKEAASGVDIFRIFDALNDVDSQMRPA 660
 QY 678 IDAVLENTNVAFAVAMAYSGDLSDPNEKLYTDYLLKMAEEIVKSGAHILAIDKMAGLLR 737
 Db 661 IDAVLENTNVAFAVAMAYSGDLSDPNEKLYTDYLLKMAEEIVKSGAHILAIDKMAGLLR 720
 QY 738 PAAVTKLVTALRREFDLPVHVTHDTAGGOLATYFAAAGADAVDVGASAPLSGTTSPS 797
 Db 721 PAAVTKLVTALRREFDLPVHVTHDTAGGOLATYFAAAGADAVDVGASAPLSGTTSPS 780
 QY 798 LSAIVAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 857
 Db 781 LSAIVAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 840
 QY 858 SNLRAGATAGLADRELLIEDNYAANVEMLRPTKVTPSSKVVGDIALHLVAGVDPAF 917
 Db 841 SNLRAGATAGLADRELLIEDNYAANVEMLRPTKVTPSSKVVGDIALHLVAGVDPAF 900
 QY 918 AADPQKIDYIPDSVIAFLRGELNPGGWPPEPLRTRALEGRSGKAPLTVPEEQAHLDA 977
 Db 901 AADPQKIDYIPDSVIAFLRGELNPGGWPPEPLRTRALEGRSGKAPLTVPEEQAHLDA 960
 QY 978 DDKERNLSNLRLPKPTEEFLEHRRRFGNTSALDDREFFYGLVGEGETLRLPDVRRP 1037
 Db 961 DDKERNLSNLRLPKPTEEFLEHRRRFGNTSALDDREFFYGLVGEGETLRLPDVRRP 1020
 QY 1038 LLVRLDAISEPDGKGRNVVAVNGQIRPMRVDRSVEVSTATAEKAADSSNKGHVAAPPA 1097
 Db 1021 LLVRLDAISEPDGKGRNVVAVNGQIRPMRVDRSVEVSTATAEKAADSSNKGHVAAPPA 1080
 QY 1098 GVVTVTAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERYVVPAAATKVEGGDLIVVYS 1157
 Db 1081 GVVTVTAEGDEVKAGDAVAIIEAMKMEATITASVDGKIDRVVVPAAATKVEGGDLIVVYS 1140

RESULT 10

ARB83180
 ID AAB83180 standard; Protein; 1139 AA.

AC XX
 AC AAB83180;

DT 09-JUL-2001 (first entry)

DE XX
 DE Corynebacterium thermoaminogenes pc protein.

XX Corynebacterium; thermophilic; amino acid biosynthesis; enzyme;
 KW thermotolerant; aceA; accBC; dtsR1; dtsR2; pfk; scrB; gluABCD;
 KW pdhA; pc; ppc; acn; icd; lpd; odhA.

OS Corynebacterium thermoaminogenes.

XX WO200125447-A1.

PN 12-APR-2001.

PD 04-OCT-2000; 2000WO-JP06913.

XX 04-OCT-1999; 99JP-0282716.

PR 01-NOV-1999; 99JP-0311147.

PR 21-APR-2000; 2000JP-0120687.

XX

PA (AJIN) AJINOMOTO CO INC.

XX Hirano S, Nonaka G, Matsuzaki Y, Akiyoshi N, Nakamura K, Kimura E;
 PI Osumi T, Matsui K, Kawahara Y, Kurahashi O, Nakamatsu T;
 PI Sugimoto S;

XX WPI; 2001-300170/31.

DR N-PSDB; AAF87437.

XX Proteins and their DNA useful for microbial production of L-amino acids

PT -

XX Claim 9; Page 132-135; 215pp; Japanese.

XX The present sequence is provided in a specification relating to genes
 encoding thermophilic amino acid biosynthesis system enzymes of
 CC the thermotolerant bacterium Corynebacterium thermoaminogenes.
 CC The novel proteins retain at least 30% isocitrate lyase activity
 CC after heating at 500C for 5 minutes. DNA fragments encoding the
 CC enzymes were isolated from a Corynebacterium thermoaminogenes
 CC chromosomal DNA plasmid library by PCR. The DNA may be used for
 CC developing strains of amino acid producing microorganisms.

XX Sequence 1139 AA;

Query Match 90.4%; Score 5299.5; DB 22; Length 1139;
 Best Local Similarity 90.9%; Pred. No. 0;
 Matches 1036; Conservative 44; Mismatches 59; Indels 1; Gaps 1;

QY 18 VSTHTSSTLPAPFKKILVANRGEIYAVRAFAALETGAATVAIYPRDRGSHFSPASEAVR 77

Db 1 VVTFPTSTLPAPFKKILVANRGEIYAVRAFAALETGAATVAIYPRDRGSHFSPASEAVR 60

QY 78 ICTGSPVKAYLIDDEIIIGAAKKKADALYPGYGSENAQALARECAENGITFIPTPEV 137

Db 61 ICTGSPVKAYLIDDEIIINAAKKKADALYPGYGSENAQALARECAENGITFIPTPEV 120

QY 138 LDLTGDKSRVTAANKAGLPVLAESTPSKNIDDIIVKSAEGQYPIFVKAVAGGGGMRMF 197

Db 121 LDLTGDKSKAVSAAKAGLPVLAESTPSDIDEIVKSAEGQYPIFVKAVAGGGGMRMF 180

QY 198 VSSPELRLKATEASREAAAFDGSVYVERAVINPOHLEVOILGDRCEVYHLERDCS 257

Db 181 VEKPELRLKATEASREAAAFDGSVYVERAVINPOHLEVOILGDRCEVYHLERDCS 240

QY 258 LQRRHQKVVEIAPQAHLDPEDLRICADAVKFCRSIGYAGTVEFLVDEKGNHVFIEKN 317

Db 241 LQRRHQKVVEIAPQAHLDPEDLRICADAVKFCRSIGYAGTVEFLVDEKGNHVFIEKN 300

QY 318 PRIQVEHTVTEETVLDLVKAQMLAAGATLKGELGTQDKIKTHGAALQCRITTEDPNN 377

Db 301 PRIQVEHTVTEETVLDLVKAQMLAAGATLKGELGTQDKIKTHGAALQCRITTEDPNN 360

QY 378 FRPDTGTTAVRSPGGAGVRLDGAALGGEITAHFDSMLVKTCRGSDFETAVARAQAL 437

Db 361 FRPDTGTTAVRSPGGAGVRLDGAALGGEITAHFDSMLVKTCRGSDFETAVARAQAL 420

QY 438 AEFVSVGATNIGFLRALLREEDFTSKRIATGFIADHSHLLQAPPADDEQGRILDIADY 497

Db 421 AEFVSVGATNIGFLRALLREEDFTSKRIATGFIADHSHLLQAPPADDEQGRILDIADY 480

QY 498 TVNKPGRVPRKVAAPIDKLPNIKDLPLPRGSRDLKQLGPAFAFARDLRQDALAVTDIT 557

Db 481 TVNKPGRVPRKVAAPIDKLPNIKDLPLPRGSRDLKQLGPAFAFARDLRQDALAVTDIT 539

QY 558 FRAHQSLLATRVRSFALKAFAAVALKIPPELLSVEAGGATYDVAMRFLFEDPWRDLDE 617

Db 540 FRAHQSLLATRVRSFALKAFAAVALKIPPELLSVEAGGATYDVAMRFLFEDPWRDLDE 599

QY 618 LREAMPNVIOMLLRGNTVGYTPYDPSVCRAFPVKEAASGVDIFRIFDALNDVDSQMRPA 677

Db 600 LREAMPNVIOMLLRGNTVGYTPYDPSVCRAFPVKEAASGVDIFRIFDALNDVDSQMRPA 659

678	QY	IDAVLETTNTAAVEAMAYSGDLSDPNPEKLYTLDYILKMAEELVYKSGAHILAIKDMAGLLR	737
660	Db	IDALETGTGTSVAEAMAYSGDLSNPCEKLYTLDYILNLAEQIVDSGHHILAIKDMAGLLR	719
738	QY	PAAVTKLVTLALRREFDLPVHVHHTDTAGGQLATYFAAAQAGADAVDGASAPLSGTTSQPS	797
720	Db	RAAAPKLVTALRREFDLPVHVHHTDTAGGQLATYFAAANAGADAVDAASAPLSGTTSQPS	779
798	QY	LSAIVAFAFTRDRTGLSLAEAVSDLEPEYWEAVRGLYLPPESGTPGPTGRVYRHEIPGGQL	857
780	Db	MSAIVAFAFTRDRTGLNLQAVSDLEPEYWEAVRGLYLPPESGTPGPTGRVYRHEIPGGQL	839
858	QY	SNLRAQATALLGLADREFELIEDNTAAVNEMLGRPTKVTPSSKVVYGDIALHLVAGVDPADF	917
840	Db	SNLRAQAVALLGLADREFELIEDYAAVNEMLGRPTKVTPSSKVVYGDIALHLVAGVSPEDF	899
918	QY	AADPQKYDIPDSVIAFLRGLGNPPGGWPEPLTRALEGRSEKGAFLTEVPEEQEAHLDA	977
900	Db	AADPQKYDIPDSVIAFLRGLGTPPGGWPEPLTRALEGRSQGKAPLAEIPAEEQAHLDS	959
978	QY	DDSKERRNSLNRLLEPKPTEEFLEHRRRGNTSALDDREFFYGLVGRETLRLPDVRTP	1037
960	Db	DUSAERGTNLNRLLEPKPTEEFLEHRRRGNTSALDDREFFYGLKEGREELIRLTGVSTP	1019
1038	QY	LLVRLDAISEPDDKGMNRNVVANYNGOIRPMKVRDRSVESVTATAEKADSSNKGHVAAPFA	1097
1020	Db	VVRLDAVSEPDKGMNRNVVANYNGOIRPIKYDRDSVESVTATAEKADATNKGHVAAPFA	1079
1098	QY	GVVTVTVAGDEVKAGDAVAITAEKMEATITASVDGKIETRVVVVPAATKVEGGDLIVVYS	1157
1080	Db	GVVTVTVAGDEITKAGDAVAITAEKMEATITAPVDGVIDRVVPAATKVEGGDLIVVYS	1139
RESULT 11			
AAB79302			
ID	XX	AAB79302 standard; Protein; 532 AA.	
AC	XX	AAB79302;	
DT	XX	30-APR-2001 (first entry)	
DE	XX	Corynebacterium glutamicum SMP protein sequence SEQ ID NO:120.	
KW	XX	Corynebacterium glutamicum; carbon metabolism and energy production;	
KW	XX	SMP protein; sugar metabolism and oxidative phosphorylation protein;	
KW	XX	fine chemical production; organic acid; proteinogenic amino acid;	
KW	XX	nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;	
KW	XX	nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;	
KW	XX	carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;	
XX	XX	diagnosis; Corynebacterium diphtheriae; evolutionary study.	
Corynebacterium glutamicum.			
OS	XX		
PN	XX	WO200100844-A2.	
PD	XX	04-JAN-2001.	
PF	XX	23-JUN-2000; 2000WO-IB00943.	
XX	XX		
PR	XX	25-JUN-1999; 99US-0141031.	
PR	XX	08-JUL-1999; 99DE-1031412.	
PR	XX	08-JUL-1999; 99DE-1031413.	
PR	XX	08-JUL-1999; 99DE-1031419.	
PR	XX	08-JUL-1999; 99DE-1031420.	
PR	XX	08-JUL-1999; 99DE-1031424.	
PR	XX	08-JUL-1999; 99DE-1031428.	
PR	XX	08-JUL-1999; 99DE-1031431.	
PR	XX	08-JUL-1999; 99DE-1031433.	
PR	XX	08-JUL-1999; 99DE-1031434.	
PR	XX	08-JUL-1999; 99DE-1031510.	
PR	XX	08-JUL-1999; 99DE-1031562.	
PR	XX	09-JUL-1999; 99DE-1031634.	
PR	XX	09-JUL-1999; 99DE-1032180.	

Db 241 LGDHTGEVHLXERCSLQRRHQKVVETAPAGHDPDLDRICADAVKFCRSIGYGGAGT 300
 QY 301 VEFILNDEKGNHVF IEMNPRIQVEHTVTEVTEVDLVKAQMRLAAGATLKEGLTQDKIKT 360
 Db 301 VEFILNDEKGNHVF IEMNPRIQVEHTVTEVTEVDLVKAQMRLAAGATLKEGLTQDKIKT 360
 QY 361 HGAALQCRITTTEDPNNRFRPDGTITATYRSPGGAGVRLDGAALGGEITAHFDSMLVKMT 420
 Db 361 HGAALQCRITTTEDPNNRFRPDGTITATYRSPGGAGVRLDGAALGGEITAHFDSMLVKMT 420
 QY 421 CRGSDFEFETAVARAQALAEFTVSGVATNIGFLRALLREDEFTSKRIATGFIGDHPHLLQA 480
 Db 421 CRGSDFEFETAVARAQALAEFTVSGVATNIGFLRALLREDEFTSKRIATGFIGDHPHLLQA 480
 QY 481 PPADDEQGRILDYLDVTVNKGPHGVRPKDVAAPIDKLPNIKDLPLPRGRSRR 532
 Db 481 PPADDEQGRILDYLDVTVNKGPHGVRPKDVAAPIDKLPNIKDLPLPRGRSRR 532

RESULT 12

AAU00511 standard; Protein; 1148 AA.

AAU00511;

07-SEP-2001 (first entry)

Bacillus subtilis pyruvate carboxylase enzyme A.

Pyruvate carboxylase A; pycA; oxaloacetate; Escherichia;

L-amino acid production; fermentation.

Bacillus subtilis strain 168.

EP1092776-A1.

18-APR-2001.

05-OCT-2000; 2000EP-0121763.

14-OCT-1999; 99RU-0121636.

(AJIN) AJINOMOTO CO INC.

Gusvatiner MM, Kozlov VI, Ptityn LR, Altman IB, Voroshilova EB;

Iomantas YAV, Yampolskaya TA;

WPI; 2001-309819/33.

N-PSDB; AAS01509.

New bacterium from the genus Escherichia containing a gene encoding for pyruvate carboxylase useful for producing higher concentrations of L-amino acids

Claim 4; Page 17-21; 28pp; English.

The present sequence represents Bacillus subtilis pyruvate carboxylase enzyme A. The pycA gene encodes for pyruvate carboxylase which catalyses the carboxylation of pyruvate to form oxaloacetate. Transformation of the Bacillus subtilis pycA gene into a bacterium belonging to the genus Escherichia results in the bacterium showing L-amino acid productivity. The invention provides a novel method for producing an L-amino acid by fermentation. The method involves cultivating the bacterium in a medium and producing and accumulating the L-amino acid in the medium. The new bacterium harbouring the gene coding for an enzyme having pyruvate carboxylase activity is useful for producing higher concentrations of L-amino acids in vitro than prior art.

Sequence 1148 AA;

Query Match 43.1%; Score 2530; DB 22; Length 1148;

Best Local Similarity 46.0%; Pred. No. 2.5e-179;
 Matches 533; Conservative 188; Mismatches 390; Indels 48; Gaps 13;
 QY 28 AFKILVANRGIAVRAFAALETGAATVAIYIPREDRSGSFHRSFAEAVRICTEGSPVKA 87
 Db 5 STQKVLVANRGIAVRAFAALETGAATVAIYIPREDRSGSFHRSFAEAVRICTEGSPVKA 87
 QY 88 YLDIEIIIGAARKKADAIYPGYFELSENAQALARECAENGITFICTPPEVLDTGDKSRA 147
 Db 65 YLDIEIIIGAARKKADAIYPGYFELSENAQALARECAENGITFICTPPEVLDTGDKSRA 147
 QY 148 VTAANKAGLVPVLAEST-PSKNIDDDIVKSAEGOTYFIFKAVAGGGRGMRVSSDELK 206
 Db 125 REQAKAGLVPVLAEST-PSKNIDDDIVKSAEGOTYFIFKAVAGGGRGMRVSSDELK 206
 QY 207 LATEASRAEAAAFGDGVSVERAVINPOHIEVQILGDRTEVGVHLEVERDCSLQRHOKVV 266
 Db 185 AYERAKSEAKAAGFNGEYVEKLIENPKHIEVQILGDRTEVGVHLEVERDCSLQRHOKVV 266
 QY 267 ETAPQAHLDPDLRICALADAVKFCRSIGYGGAGTVEFVDEKGNHVF IEMNPRIQVEHTV 326
 Db 245 EVAPSVLSPELDQICEAAVALAKNVNINAGTVEFLV-ANNEFFYFIEVNPVQVEHTI 303
 QY 327 TEEVTEVDLVKAQMRLAAGATL--KELGLTQDK--IKTHGAALQCRITTTEDPNNRFRPDG 383
 Db 304 TEEVTEVDLVKAQMRLAAGATL--KELGLTQDK--IKTHGAALQCRITTTEDPNNRFRPDG 383
 QY 384 TITAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTV 442
 Db 364 KIMAYRSPGGAGVRLDGTNSFOGAVITPYDLSLLVKLSTWALTPEQAAKVMYRNQEFRI 423
 QY 443 SCVATNIGFLRALLREDEFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLDVTVN-- 500
 Db 424 RGIKTIPELENVAKHEKFLTGQYDTSFIDTTPPELFNFPKQKDRGKMLTYIGNTVNGF 483
 QY 501 -----KPHGVPRPKDVAAPIDKLPNIKDLPLPRGRSRRDLKOLGPAAPARDLEODALAV 553
 Db 484 PGIGKKEKPAEDKPLGVKVDVQDP-----ARCTKQILDEKGAAGLANWVKEQSVLL 536
 QY 554 TDTTFRDAHQSLLATRVRSFALPAAEAVAKITPELLSVEAMGGATYDVAMRFLFEDPMD 613
 Db 537 TDTTFRDAHQSLLATRVRSFALPAAEAVAKITPELLSVEAMGGATYDVAMRFLFEDPMD 613
 QY 614 RLDELREAMPVNIQMLLRGNTVGYTPYDPSVCFRAFKEAASSVDIFRFDALNDVSO 673
 Db 597 RLEDLRKEVPNTLFQMLLRSSNAVGYTNPONVIKEFYKQSAQSGIDVFRFIDSLNWYKG 656
 QY 674 MRPAIDAVLENTAVAEVAMAYSGDLSDPNEKLYTLDYLLKMAEIVKSGAHILAIKDMA 733
 Db 657 MTLAIDAVRDGT-KVAEAAICYTGDILDKNRTKYDLAYTTSMAKLEAAGAHILAIKDMA 715
 QY 734 GLLRPAAVTKLVTLRREFDLPVHVHTDITAGGQATYFAAAQAGADAVDGASAPLSGTT 793
 Db 716 GLLRPAAVTKLVTLRREFDLPVHVHTDITAGGQATYFAAAQAGADAVDGASAPLSGTT 793
 QY 794 SOPSLSAIVAAFAHTRDITGLSLEAVSDLEPYWEAVRGLYLPFESGTPGTVRHRHIP 853
 Db 776 SOPSLSAIVAAFAHTRDITGLSLEAVSDLEPYWEAVRGLYLPFESGTPGTVRHRHIP 853
 QY 854 GGQSLNRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTSSKVVGDALHLVAGVD 913
 Db 836 GGQSLNRAQATALGLADRFELIEDNYAAVNEMLGRPTKVTSSKVVGDALHLVAGVD 913
 QY 914 PADFAADPQKVDIPDSVIAFLRGELGNPPGWPPELRLTRALEGSEKAPITEVEPEE--- 970
 Db 896 EKDVYKESGLDPPDSVVVELFKGNIGQPHGGFPEKQLKILKQGE---PITVRPGELLE 951
 QY 971 -----EQAHLDAADDKERNLSNLLFPKTEPEELRRRFGNTSALDDREFF 1018
 Db 952 PVSFEAIKQEFKEQHNEISD-----QDAVAYALYKPYFTDYVKTTSYGLSILDTTFF 1007
 QY 1019 YGLVEGRETLIRLPDVRTPELILVRLDAISEPDKGMNVNANVNGQIRPMRVDRSVESVT 1078

Db	1008	YGMTLGEIEVEIERGKT-LIVKILISIGEPQDATTRVVFELNGQPREVVIKDESIKSV	1066
QY	1079	ATAEKADSSNKGHVAFAGVWTVVAE-GDEVKAGDAVAIIEMAKMEATITASVQKIE	1137
Db	1067	QERIKADRTNPSHIAASMPGTIVIKVLAEGTKYNGDHLMINAMKMETTVAPFSTGIC	1126

QY	1138	RVVPAATKVEGGDLIVV	1156
		: : :	
Db	1127	QVHVKNGEPIQTGDLLEI	1145

RESULT 13

RESULT 13
ABB47612
ID ABB47612 standard; Protein: 1146 AA;

XX
AC ABB47612:

DT 05-FEB-2002 (first entry)

Listeria monocytogenes protein #316.

KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.

OS *Listeria monocytogenes*.

PN WO200177335-A2.

18-OCT-2001.
PD
XXXX
PF
11-APR-2001:

11-APR-2000: 2000FR-0004629

XX PA (INSP) INST PASTEUR

XX Buchrieser C. Franco

PI Dussartel O, Cretouani F, Negjari H, Glaser P, Kunst F, Cossart
PI Daniels J, Goebel W, Krest J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Hierrez-Martinez A, Amend A,
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablos B, Wehlund J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;

AA
DR WPI; 2002-010914/01.

Genomic sequence for *Listeria* monocytogenes, useful e.g. for treatment and prevention of *Listeria* and related bacterial infections, and related polypeptides -

PS Claim 6; SEO ID No 317; 192pp; French
XX

The present invention relates to the genome sequence of *Listeria monocytogenes* EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in *L. monocytogenes* and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of *L. monocytogenes* and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate *L. monocytogenes*-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by *L. monocytogenes* and related organisms.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pat_sequences](ftp:wipo.int/pub/published_pat_sequences).

Sequence 1146 AA;

Query Match	42.5%	Score 2494;	DB 23;	Length 1146;
Best Local Similarity	45.7%;	Pred. No. 1.2e-176;		
Matches 525;	Conservative 186;	Mismatches 408;	Indels 30;	Gaps 11

QY 30 KILVANRGETIAVRAALETGAATVAIYPREDGRGSHRSFASEAVRIGTEGSPVKAYL 89
||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||
||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|||||

3 RAVLVANRGEIAIKVWKACTELKIKTVAILYQEDTGSFHRYKSD EAYLVAGAGKKPIDAYL 64
 QY 90 DIDEIIGAKKKVKADALYPGYGTFSENAOLARECAENGTIFIGTPEVLDLTGDKSRVTT 149

Db 65 DIENLIEAKESGADATHPGYGFELSENIEFARCEQEGIFVGPXSKHLMFGDKIKAKE 124

[illegible]

QY 209 TEASREAEAFGDGSSVVERAVINPQHIEVQILGDRTEGVVHLVERDCSLQRHQKVVEI 268

DB 185 ERASSEAKAAGNDEYVEKCVMPKHFVQILGDTGHNIVHLFERDCSIQRHQKVEV 244

QW 269 ADKQHI DREI DDYDNDAAVDDGCTGVQKSGHUPPTDGNKNNVDTFANQVQVVEV 300

Db 245 APCNAITSELNRICDAAVKLMKNVDYINACTVEFLV-EGDDFFFLYEVNPRQVEHTITE 303

```
QY      329 EVTEVDLVKAQMRLAAGATLKELGLT---QDKIKTHGAALQCRTITEDPNNGRPDGTG 385
```

QY 386 TAYRSPGAGVRLD-GAAQLGCEITAHFDSMLVKVTCRGSDPETAVARAQALAEFTVSG 444

Db 364 DTYRSTGGFGVRLDAGNGFQGTWVTPFYDSLVLKLVCLCTWGMTFEQATRKMRNLIEFRING 423

db 424 VKTNIPFLNVVRHDPFASGNVNTSFIDTPELFKEPHIRDRGKTKLRYGNVTVNGPPG 483

```
QY 505 VRPKDVAAPIDKLPNIKDLP----LPRGSRDRLKQIGPAAFAARDLREQDALAVDTTFRD 560
```

404	IAHND--AFVIAEPRFKPIPGSQISPGTKQILLDANGPEGVDMWVKRQKEEVLTTDLRD	541
561	AHQSLIATRVRSFALKPAAEAAVAKLTPELLSVEANGGATYDVAMRELFEDEPWDRIDEIRE	620

Db 542 AHQSLLATRVRSKDIFFQVADAMAHLLPNMFSEFMGGATFDVAYRFLNEDPVRLEIRK 601

QY	021	AMPNVNQLMLLRGNVTGTYTFYPDSVCRAFAVKEAASSGVDFRIFDALNDVDSQMRPADA	681
Db	602	QIPNVMEQMLLRGNNAVGYKNYPDNVIREFVKOSAOSGVDFVERFDSIWNIIKGMVEVSDA	661

QY 681 VLETNTAAVEAMAYSGDLDSPNEKLYTLDDYLLKMAEEIVKSCAHILATKDMAGLLRPAA 740

D6	662	VREAG-KWEEAATCYGDI	DDDTTRTKYRIDYYKDMAKELVAQ	QTHILGDKMAGLLKPQA	720
QV	741	VTKLVTALRREEDLPVHVH	THDTAGGQIATYFAAACAGADAYDCA	SAPISGTTT	SOBSISA 800

Db 721 AYRLIGELKDTVDVPIHLHFTDTSNGIYTYAAAVSAGVDIVDVASSANGSATSQPSMTG 780

801 IVAAFAHTRDTCISLEAVSDLEPYWEAVRGLYLPFFESGTPGPTGRVYRHEIPGGGLSNI 860

QY 861 RAQATAGLADRFELIEDNYAAVNEMIGRP TKVTPSSKVVGDLALHLVGAGVDPAADFAAD 920

Db 841 QQQATAVGLGDRWDEVKEMYTIVVNQMGFDIVKVTPTSSKVVGDIALFMVQNELSEEDVYEK 900

Db 901 GDTIDPDSVIEFMGEICQPYGGFFPEKLOKLVLKGR-----PLTDRGAIMEPYVFDV 956

QY 981 K-----ERRNSLNRLLPKPTTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLI 1029

95 / KAELEKMGIEPTERKDVISYLLIPKVFLDYQDMINKYGDVTVLDTPTFYKGMRLGETIEV I010


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Db 941 LTARPEYLEPVDFEKVELLEEQGPVTEQDIISVLYPKVYEQYIQTRNQGNSLL 1000
Qy 1013 DOREFFYGLVGRRETLRLPDRVPLVRLDAISEPDDKGRNVVANYNGQIRPMVRDR 1072
Db 1001 DTPFFFGMRNGETVEIEI-DGKRLLIKLEITISEPDENGRTIYIYAMNGQARRIYIKDE 1059
Qy 1073 SVESYATAEAKDSNGKHVAAPFAGVVT-VTVAGDEVKAGDAVAIIIEAMKMEATITAS 1131
Db 1060 NVHTNANVYKPRADSNPSHIGAQMPGVSVEYKVSGETIVKANQPLLIIEAMKMETTIQAP 1119
Qy 1132 VDGKIERVVVPAATKVEGGDLIVV 1156
Db 1120 FDGVIKQTVNNGDTIATGDLLEI 1144

```

RESULT 15

```

AAG82677
ID AAG82677 standard; Protein; 1151 AA.
XX AC AAG82677;
XX DT 03-SEP-2001 (first entry)
XX DE S. epidermidis open reading frame protein sequence SEQ ID NO:2448.
XX KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
XX KW vaccination; endocarditis.
XX OS Staphylococcus epidermidis.
XX PN WO200134809-A2.
XX PD 17-MAY-2001.
XX PF 09-NOV-2000; 2000WO-US30782.
XX PR 09-NOV-1999; 99US-0164258.
XX FA (GLAX ) GLAXO GROUP LTD.
XX PI Kimmerly WJ;
XX DR WPI; 2001-316495/33.
XX DR N-PSDB; AAH53527.

Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
useful for vaccinating against infections, e.g. endocarditis -

Claim 18; Page 644-645; 2188pp; English.

AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides
(II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.
(I) and (II) can have antibacterial activity and therefore can be used
in vaccination. The nucleic acids (I) may be used to produce the
S. epidermidis polypeptides (II) via the production of vectors
containing them which are used to produce hosts cells which express the
polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
used to vaccinate subjects and to raise antibodies against the bacteria.
The polypeptides may also be used to assay for other inhibitors of their
activity and therefore identify compounds that may be used for the
treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
AAH55090 represent specifically claimed S. epidermidis genomic DNA
polynucleotide sequences from the present invention. AAH55091 to
AAH55098 represent oligonucleotide sequences and primers which are used
in the exemplification of the present invention.
N.B. The present invention specifically claims all the polynucleotide
sequences given in the sequence listing of the present specification,
however the sequence listing only goes up to SEQ ID NO:4454 so even
though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
no sequences are present for SEQ ID NO:4455 to 4464.

Sequence 1151 AA;

```

```

Query Match 42.0%; Score 2465; DB 22; Length 1151;
Best local Similarity 45.4%; Pred. No. 1.8e-174;
Matches 524; Conservative 198; Mismatches 399; Indels 34; Gaps 14;

Qy 26 LPAFKIILVANGETAVRAAALGTGAATVAIYREDRSGSPHRGFASAVRIGTEGSPV 85
Db 5 LKQIKLLVANGETAIRFRAAELNSTVAIYSNEDKSSLHRYKADESILYVGSGLGPA 64
Qy 86 KAYLIDIEIGAAGKVKADAIYGYGFLSENQAALRECAENGITFIGPTPEVLDITGKS 145
Db 65 ESYLNIERIIEVALRAGVDAIHGPGYGLSENQFAARCAEEGKITGPHLEHDMFGDKV 124
Qy 146 RAVTAARKAGLPVL-AESTPSKNIDIVKSBGGQYPIFVKAVAGGGRGMRFFVSPDEL 204
Db 125 KARTAINANLPVPIPTGDPGPIESFEAAEQFANEAGYPLMIKATSGGGGKMRIVRESSEL 184
Qy 205 RKLATEASREAEAAFGDGVVYVERAVINPQIHTEVOILGDRTEGVVHLYERDCSLQRHQK 264
Db 185 EDATFRKASEAKSFGNSEVYIERIDNPKHIEVOIGDEFGNIHLHYERDCSVQRHQK 244
Qy 265 VVEIAPAOHLDELDRICADAVKFCRISIGYGGAGTVEFLV--DEKGNHVFIEMPRIQV 322
Db 245 VVEVAPSVGLSKLKRERICDAAIQIMENIKYVNACTVEFLVSGDE---FFIEVNPVQV 301
Qy 323 EHTVTEEVTEVDLVKAQMLAAGATL---KELGLTODKIKTHGAALOCRIITEDPNNGFR 379
Db 302 EHTITEMITGIDIVKTQILVADGESLFGDKLSMPOONEIQTILGYAICRIITEDTNDFM 361
Qy 380 PDTGTITAYRSPGGAGVRID-GAAQLGGEITAHFDSMLVKMTCRGSDSETAVARAALA 438
Db 362 PDSGTIIAYRSSGGFVRLDAGDGFGQAEISPYDLSLVKLSTHAVSFKAEEKMERSUR 421
Qy 439 EFTVSGVATNIGFLRALLREEDFTSKRIATGIGDHPHLLQAPPADDDQGRILDYADVT 498
Db 422 EMIRGVKINIPFLINVMRNDKFRSGDYTTFTFETPELFIAPLDRGTILTEYIGNVT 481
Qy 499 VNKPHGV--RPKQVAAPIDKLPNKIDPLPR--GSRDLKQLGPAFAAFARDLREODALAVT 554
Db 482 INGFNPVEKRPK- EYESTKIPKISOKKINQLFGTKQILEQHGPTGVTVNWREQEDVLIT 540
Qy 555 DTTFRDAHQSLLATRVRSFALKPAEAAVAKITPELLSVEANGGATYDYAMRFLFEDPWR 614
Db 541 DTTFRDAHQSLLATRVRTKDMNTASKTAEVFKDSFSELMWGGATFDVAYNFLKENPWER 600
Qy 615 LDELREAMPNVIOMLLRGRNTVGYTPYDPSVCRAFVKEAASSGVVDIIFRIDALNDVSCM 674
Db 601 LERUKAIPNVLFQMLLRASNAVGYKNYPORNVIKKFVHESAKAGVDVFRIFDSLNWVDQM 660
Qy 675 RPAIDAVLENTNTVAEAMAYSGD--LSDPNEKLYTLDYLLKMAEIVKSGAHILAIDKMA 733
Db 661 KVANEAVQEQAG-MVSEGTICVTGDLINAEERNITLDYVVKMAKLEREGPHILAIDKMA 719
Qy 734 GLLRPAAVTKULVALRREFDLFPVHVHDTAGGOLATYFAAAQAGADAVDGASAPLSTGT 793
Db 720 GLLPKAAEYELIGELREATHLPILHLTHTDSNGLLATYKQAIADAGVDIIDTAVASMSLT 779
Qy 794 SOPSLSATVAFAHTRDRDTGLSLEAVSDLEPYWEAVGLXLPESGTPGPTGVYRHEIP 853
Db 780 SOPSANSIYYALNGFPRLRTRTDIDGLELSHWSVVRPYADPFESDKSPNTEIYQHEMP 839
Qy 854 GGQSLNLRQAQATLGLADRFELIEDNYAAVNEMLGRPTKVTPTSSKVVYGDALHLVAGVD 913
Db 840 GGQVSNLSQQAQSLGLGERDEVEKMYRRVNFGLVKVTPSSKVVGDMAIYVQNDLD 899
Qy 914 PADFAADPKYDIPDSVIAFLRUGELGNPPGWPPELRLTRALEGRSEKAPUTEVEPEQA 973
Db 900 EDTVINDGYKLDPEPSVSVFFKDGIPGVNGFNKKLQDVILKQQQ----PITERPGEYLE 955
Qy 974 HLDAD-----DSKERNSLNRLLEPKPTEEFLEHRRRGNTSALDDRRFFFGVLV 1022
Db 956 PVDFEATRQELSDIQDEVTEQDIISVLYPKVYEQYIQTRKQFGNVSLLDTPITFLGMR 1015

```

QY 1023 EGRETLRLPDPVTPLLVRLDAISEPDDKGRNVVAVNNGQIRPMRVDRSVESTATAE 1082
 Db | : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
 1016 NGTVELEI-DTGRLLIIKLETISEPDENGKRTIYYAMNGQARRIYIQDENVKTANVKP 1074
 QY 1083 KADSSNKGHVAAFPAGVVT-VTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIERVVV 1141
 Db ||| || | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 1075 KADKSNPNHIGAOMPGSVTEVKYSVGDEVQANQPLIITEAMKMETTIQAPFDGLIKQINV 1134
 QY 1142 PAATKVEGGDLIVV 1156
 Db : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 1135 ANGDAIATGDLLEI 1149

Search completed: September 24, 2003, 15:55:21
 Job time : 70.4737 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 15:27:07 ; Search time 18.1332 Seconds
(without alignments)
2699.668 Million cell updates/sec

Title: US-09-974-973A-2

Perfect score: 5865

Sequence: 1 MTAITLGLLLKGIITVST.....RWVPAATKVEGDLIVVVS 1157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5759	98.2	1140	3	US-09-220-081-2
2	5759	98.2	1140	4	US-09-677-575-2
3	3484	59.4	1124	4	US-08-311-731A-10
4	2465	42.0	1154	4	US-09-134-001C-3428
5	2182	37.2	973	4	US-09-107-532A-4810
6	1192	20.3	694	4	US-09-433-043B-126
7	1084	18.5	456	4	US-09-634-238-276
8	1039.5	17.7	593	4	US-09-433-043B-122
9	1032.5	17.6	447	1	US-08-611-107-6
10	1032.5	17.6	447	2	US-08-422-560A-6
11	1032.5	17.6	447	3	US-08-468-793-6
12	1005.5	17.1	453	1	US-08-611-107-8
13	1005.5	17.1	453	2	US-08-422-560A-8
14	1005.5	17.1	453	3	US-08-468-793-8
15	1003.5	17.1	453	4	US-09-433-043B-121
16	996.5	17.0	453	1	US-07-956-700B-6
17	996.5	17.0	453	1	US-08-476-537-6
18	996.5	17.0	453	1	US-08-485-607-6
19	996.5	17.0	453	2	US-08-475-879-6
20	996.5	17.0	453	4	US-09-433-043B-6
21	973	16.6	474	4	US-09-328-352-7562
22	964.5	16.4	1116	4	US-09-252-991A-24374
23	954	16.3	605	4	US-08-433-043B-123
24	940	16.0	448	1	US-08-074-121-3
25	940	16.0	448	5	PCT-US94-06447-3
26	937.5	16.0	454	4	US-09-198-452A-197
27	937.5	16.0	701	4	US-09-252-991A-27999

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28 933 15.9 427 1 US-07-956-700B-3 Sequence 3, Appli
29 933 15.9 427 1 US-08-476-537-3 Sequence 3, Appli
30 933 15.9 427 1 US-08-485-607-3 Sequence 3, Appli
31 933 15.9 427 2 US-08-475-879-3 Sequence 3, Appli
32 933 15.9 427 4 US-09-433-043B-3 Sequence 3, Appli
33 928 15.8 536 3 US-08-662-344-2 Sequence 2, Appli
34 921.5 15.7 465 4 US-09-252-991A-26980 Sequence 26980, A
35 921 15.7 449 1 US-08-074-121-6 Sequence 6, Appli
36 921 15.7 449 5 PCT-US94-06447-3 Sequence 6, Appli
37 910 15.5 676 4 US-09-252-991A-26143 Sequence 26143, A
38 902 15.4 670 4 US-09-328-352-6725 Sequence 6725, Ap
39 892 15.2 652 4 US-09-328-352-5587 Sequence 5587, Ap
40 888 15.1 573 4 US-09-328-352-6420 Sequence 6420, Ap
41 869 14.8 1212 4 US-09-252-991A-26616 Sequence 26616, A
42 849 14.5 461 4 US-09-134-001C-3604 Sequence 3604, Ap
43 843 14.4 612 4 US-09-252-991A-19134 Sequence 19134, A
44 842.5 14.4 722 4 US-09-433-043B-125 Sequence 125, App
45 832.5 14.2 453 4 US-09-252-991A-19829 Sequence 19829, A

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ALIGNMENTS

RESULT 1

US-09-220-081-2

; Sequence 2, Application US/092200081

; Patent No. 6171833

; GENERAL INFORMATION:

; APPLICANT: Sinskey, Anthony J.

; APPLICANT: Lessard, Philip A.

; APPLICANT: Willis, Laura B.

; APPLICANT: Stephanopoulos, Gregory

; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum

; FILE REFERENCE: 1533.0790000

; CURRENT APPLICATION NUMBER: US/09/220,081

; CURRENT FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 1140

; TYPE: PRT

; ORGANISM: Corynebacterium glutamicum

US-09-220-081-2

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Query Match 98.2%; Score 5759; DB 3; Length 1140;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1133; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 18 VSTHTSSTLPAPFKKILVANRGEIAVRAPRAALETGAATVAIYPRDRGSGFHRSEAVR 77
Db 1 MSTHTSSTLPAPFKKILVANRGEIAVRAPRAALETGAATVAIYPRDRGSGFHRSEAVR 60
QY 78 IGTGSPVKAYLDDDEITGAAKVKADAIYPGYGFLENAQLARECAENGITFGPTPEV 137
Db 61 IGTGSPVKAYLDDDEITGAAKVKADAIYPGYGFLENAQLARECAENGITFGPTPEV 120
QY 138 LDLTGDKSRAYTAAKKAGLPVLAESTPSKNIDDLVKSAGOTYPIFKVAGGGGRMR 197
Db 121 LDLTGDKSRAYTAAKKAGLPVLAESTPSKNIDDLVKSAGOTYPIFKVAGGGGRMR 180
QY 198 VSSDELKRLATEASREAAFGDGSVYVERAVINPQHIEVQILGDRGTGEVHHLYERDCS 257
Db 181 VASDELKRLATEASREAAFGDGSVYVERAVINPQHIEVQILGDRGTGEVHHLYERDCS 240
QY 258 LQRHOKVETAPQAHLDPRLDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFEMN 317
Db 241 LQRHOKVETAPQAHLDPRLDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFEMN 300
QY 318 PRIOVEHTVEEVDLVKQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDNNNG 377
Db 301 PRIOVEHTVEEVDLVKQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDNNNG 360
QY 378 FRDTGHTITAYRSPGGAGVRIDGAAQLGGEITTAHFDNMLVKMTCRGSDFFETAVARAQAL 437

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Db 361 FRPDGTITATYRSGGAGVRLDGAALGGGETTAHFDSMLVMTCRGSDFTAVARAQAL 420
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Db 421 AEFTVSGVATNIGFRLALLREEDFTSKRIATGFTADHPHLLQAPADDEQGRILLYADV 480
QY 498 TVNPHGVPRKDVAAIDKLPNIKDLPLPGSRDLKOLGPAAPAFARDLREQDALAVTDTT 557
Db 481 TVNPHGVPRKDVAAIDKLPNIKDLPLPGSRDLKOLGPAAPAFARDLREQDALAVTDTT 540
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Db 541 FRDAHQSLLATRVRSFALKPAEAAVAKLTPELLSVEAWGGATYDVAMRFLFEDPDWRDLDE 600
QY 618 LREAMPVNIQMLLRGRNTVGYTPYDVSVCRAFYKEAASSGVDFRIFDALNDYSQMRPA 677
Db 601 LREAMPVNIQMLLRGRNTVGYTPYDVSVCRAFYKEAASSGVDFRIFDALNDYSQMRPA 660
QY 678 IDAVLENTAVAEVAMAYSGDLSDPNEKLYTLDYLLKMAEIVKSGAHILAIDKMAGLLR 737
Db 661 IDAVLENTAVAEVAMAYSGDLSDPNEKLYTLDYLLKMAEIVKSGAHILAIDKMAGLLR 720
QY 738 PAAVTKLVTALRRREFDLPVHVHTHDTAGGQATYFAAAQAGADAVDGSAPLSGTTSPS 797
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QY 798 LSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 857
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Db 841 SNLRAQATAGLADRFELIEDNYAANVEMLRGPTKVTTPSSKVVGDALHLVGVADPADF 900
QY 918 AADPKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEKAPLITEVPEEQAHLDA 977
Db 901 AADPKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEKAPLITEVPEEQAHLDA 960
QY 978 DDSKERNLSNRLLPKPTTEFFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTP 1037
Db 961 DDSKERNLSNRLLPKPTTEFFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTP 1020
QY 1038 LLVRLDAISEPDDKGMNVANVNGQIRPMVRDRSVESVTATAEKADSSNKGHVAAPFA 1097
Db 1021 LLVRLDAISEPDDKGMNVANVNGQIRPMVRDRSVESVTATAEKADSSNKGHVAAPFA 1080
QY 1098 GWTVTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIERYVVPAAATKVEGGDLIVVVS 1157
Db 1081 GWTVTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIERYVVPAAATKVEGGDLIVVVS 1140
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RESULT 2

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US-09-677-575-2
; Sequence 2, Application US/09677575
; Patent No. 6403351
; GENERAL INFORMATION:
; APPLICANT: Sinskey, Anthony J.
; APPLICANT: Lessard, Philip A.
; APPLICANT: Willis, Laura B.
; APPLICANT: Stephanopoulos, Gregory
; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
; FILE REFERENCE: 1533.079000
; CURRENT APPLICATION NUMBER: US/09/677,575
; CURRENT FILING DATE: 2000-10-03
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
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US-09-677-575-2

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Query Match
Best Local Similarity 98.2%; Score 5759; DB 4; Length 1140;
Matches 1133; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
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Db 61 IGTEGSPKAYLDDDEIIIGAAKKYKADAIYGYGFLSENAQLARECAENGITFTGPTPEV 120
QY 138 LDLTGDKSRAYTAARKAGLPVLAESTPSKNIDDIIVKSAEGQTYPIFYKAVAGGGGRMRF 197
Db 121 LDLTGDKSRAYTAARKAGLPVLAESTPSKNIDDIIVKSAEGQTYPIFYKAVAGGGGRMRF 180
QY 198 VSSDELRKLKATEASREAAAFGDSGVYVERAVINPQHIEVQILGDRTEGTVVHLYERDCS 257
Db 181 VASPELRKLKATEASREAAAFGDSGVYVERAVINPQHIEVQILGDRTEGTVVHLYERDCS 240
QY 258 LORRHQKVEIAPACHLDPELRDRICADAVKFCRSIGYGAGTVEFFLDEKGNHVFTEMN 317
Db 241 LORRHQKVEIAPACHLDPELRDRICADAVKFCRSIGYGAGTVEFFLDEKGNHVFTEMN 300
QY 318 PRIQVEHTVTTEEVTEVDLVKAQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNNG 377
Db 301 PRIQVEHTVTTEEVTEVDLVKAQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNNG 360
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Db 361 FRPDGTITATYRSGGAGVRLDGAALGGGETTAHFDSMLVMTCRGSDFTAVARAQAL 420
QY 438 AEFTVSGVATNIGFRLALLREEDFTSKRIATGFTGDHPHLLQAPADDEQGRILLYADV 497
Db 421 AEFTVSGVATNIGFRLALLREEDFTSKRIATGFTADHPHLLQAPADDEQGRILLYADV 480
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Db 481 TVNPHGVPRKDVAAIDKLPNIKDLPLPGSRDLKOLGPAAPAFARDLREQDALAVTDTT 540
QY 558 FRDAHQSLLATRVRSFALKPAEAAVAKLTPELLSVEAWGGATYDVAMRFLFEDPDWRDLDE 617
Db 541 FRDAHQSLLATRVRSFALKPAEAAVAKLTPELLSVEAWGGATYDVAMRFLFEDPDWRDLDE 600
QY 618 LREAMPVNIQMLLRGRNTVGYTPYDVSVCRAFYKEAASSGVDFRIFDALNDYSQMRPA 677
Db 601 LREAMPVNIQMLLRGRNTVGYTPYDVSVCRAFYKEAASSGVDFRIFDALNDYSQMRPA 660
QY 678 IDAVLENTAVAEVAMAYSGDLSDPNEKLYTLDYLLKMAEIVKSGAHILAIDKMAGLLR 737
Db 661 IDAVLENTAVAEVAMAYSGDLSDPNEKLYTLDYLLKMAEIVKSGAHILAIDKMAGLLR 720
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Db 721 PAAVTKLVTALRRREFDLPVHVHTHDTAGGQATYFAAAQAGADAVDGSAPLSGTTSPS 780
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Db 841 SNLRAQATAGLADRFELIEDNYAANVEMLRGPTKVTTPSSKVVGDALHLVGVADPADF 900
QY 918 AADPKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEKAPLITEVPEEQAHLDA 977
Db 901 AADPKYDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEKAPLITEVPEEQAHLDA 960
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Db 961 DDSKERNLSNRLLPKPTTEFFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRTP 1020
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QY 1038 LLVRLDAISEPDDKGMNVVAVNGOIRPMVRDRSVESVATAEAKDSSNKGHVAAPFA 1097
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 Db 1021 LLVRLDAISEPDDKGMNVVAVNGOIRPMVRDRSVESVATAEAKDSSNKGHVAAPFA 1080
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 QY 1098 GVVTVTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIERVVVPAAATKVEGGDLIVVYS 1157
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 Db 1081 GVVTVTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAAATKVEGGDLIVVYS 1140
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RESULT 3

US-08-311-731A-10
 ; Sequence 10, Application US/08311731A
 ; Patent No. 6583266
 ; GENERAL INFORMATION:
 ; APPLICANT: SMITH, DOUGLAS
 ; APPLICANT: MAO, JEN-I
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
 ; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; NUMBER OF SEQUENCES: 411
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
 ; STREET: 600 ATLANTIC AVENUE
 ; CITY: BOSTON
 ; STATE: MASSACHUSETTS
 ; COUNTRY: USA
 ; ZIP: 02210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/311,731A
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GATES, EDWARD R.
 ; REGISTRATION NUMBER: 31,616
 ; REFERENCE/DOCKET NUMBER: C0044/7125
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/720-3500
 ; TELEFAX: 617/720-2441
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1124 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: YES
 ; ORIGINAL SOURCE:
 ; ORGANISM: MYCOBACTERIUM TUBERCULOSIS
 ; US-08-311-731A-10

Query Match 59.4%; Score 3484; DB 4; Length 1124;
 Best Local Similarity 62.2%; Pred. No. 4.6e-267;
 Matches 698; Conservative 151; Mismatches 251; Indels 22; Gaps 9;
 QY 29 FKKILVANGETAVRAFAALETGAATVAIYPRDRGSHRSFASFAVRIGTSGPVKAY 88
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 Db 2 FSKVLVANGETAIAFRAYELGVTVAIYPRDRGSHRSFASFAVRIGTSGPVKAY 61
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 Db 62 LSVDEIVATARRAGADAIYGYGFLSENPDIAAACAAGISFVGSAAEVLGAGNKSRAI 121
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 QY 149 TAAKAGLPVLAESTPSKNIDIVKSAEGQTPIFVKAVAGGGGRMRFVSSPDELKIA 208
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 Db 122 AAAREAGLPVLMSSAPSASVDELLSVAAGMPFLEVKAVAGGGGRMRFVSSPDELKIA 181
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 QY 209 TEASREAAAFDGGSVYVERAVINPQHLEVTQLIGDRTGEVHLYEDCSLQRHKKVVEI 268
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Db 182 EAASREAESAFGDPVTYVLEQAVINPRHIEVQIILADNLGDVILHLYERDCSVQRHOKVIEL 241
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 QY 269 APAQHLDPRLERIDICADAVKFCRSIGYQAGAGIVEFLVDEKGNVFTTEMPRIQVEHTVIE 328
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 Db 242 APAPHLDAELRYKMCYDAVAFARHIGYSCAGIVEFLDERGEYVFTTEMPRQVEHTVTE 301
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 QY 329 EYTEVDLVKAQRLAAGATLKEGLTQDKIKYGAALQCRITTEDPNNCFRPPDTGITYAY 388
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 Db 302 EITDVLVASQLRIAGETLEQLGRQEDIAHPGAALQCRITTEDPANFRP-TRAGSAR 360
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 QY 389 RSPGGAGYRLDGAALGGGEITAHFDSMLYKM-----TCRGSDFETAVARAQALAEFTVS 443
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 Db 361 CDPAPVPSAWTAAP-----TWRRNQPVRLHAGQADLSGRDLPATSVARRAIAEFRI 415
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 QY 444 GYATNIGFLRALLREEDFTSKRIATCFIGDHPHLLQAPPADDEQGLIYLDVTVNKP 503
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 Db 416 GYSTNIPFLOAVLDDPDFRAGRVTTSFIDERPQLTARASADRGTKILFLADVTYNNPY 475
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 QY 504 GYRPKDVAAPIDKLPNIKDPLPL----PRGSRDLKOLGPAAFARDLREQDALAVTDTTFR 559
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 Db 476 GSRPSTI-YPDDKLP---DLDLRAAPPAGSKQRLVKGEGFARWLRESAAGVTDITFR 531
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 QY 560 DAHQSLLATRVRSFALKPAEAAVAKLTPELLSVAMGATYDVAMRFLFEDPWDRLEUR 619
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 Db 532 DAHQSLLATRVRTSGLSRVAPYLARTMPOLLSVECGGATYDVALRFLKEDPWLERLATLR 591
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 QY 620 EAMPNVNIOMLLRNTVGYTPYDPSVCFRAFEASSGVDIFRIFDALNDYSQMPAID 679
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 Db 592 AAMPNIOMLLRNTVGYTPYDPSVCFRAFEASSGVDIFRIFDALNDYSQMPAID 651
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 QY 680 AVLENTAVAEVAMAYSGDSDPNEXLYTIDLYLKMAEETVKSAGHILAKDMAGLLRPA 739
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 QY 740 AVTKLVTLRRFEDLPVHVHTHTAGGQLATFAAAQAGADAVDAGSABLSGTSQPSLS 799
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 Db 712 AAQRLVSAIUSRFDLPVHLHTHTPGGQLASYAAWHAGADAVDGAAPLAGTTSQAPLS 771
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 QY 800 AIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGILYLPFESGTPGCTGRVYRHEIPGGQLSN 859
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 Db 772 SIVAAAHAETGYDTGLSVALEPYWEALRVIAFESGLPGPTGRVYRHEIPGGQLSN 831
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 QY 860 LRAQATALGLDRFELIEDNYAAVNEMLRPTKVTPSSKVVGDALHLHVAGYDPAFAA 919
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 Db 832 LRQAIALGLGDRFEIEEYAGADRVLGKLVKVTPTSKVVGDLALALVAGVSADAFAS 891
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 QY 920 DPQKYDIPDSVIAFLRGELGNPPGWPPELRLTALRSEGRKAPLITEVEEQAHLDADD 979
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 Db 892 DPAREGIPESVILGELGELGDPGMPPELRTAALAGGAAR-PTAQLAADDEIALSSVG 950
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 Db 1009 IGLAISPEDEGRMRTVMCILNGQLRPLVLRDRSTASAVPAEAKADGPNPGHIAAPFAGV 1068
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 QY 1100 VVVTVAEDEVKAGDAVAIIEMKMEATITASVDGKIERYVV 1141
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 Db 1069 VTVGVCVGRVAGGQTIATIEAMKWEAPITAPVAGTVKRVAV 1110
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RESULT 4

US-09-134-001C-3428
 ; Sequence 3428, Application US/09134001C
 ; Patent No. 6360370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C

QY	26	LP	A	F	K	K	L	L	V	N	R	G	E	I	A	V	R	A	L	E	T	G	A	A	T	V	A	I	P	R	E	D	R	G	S	F	H	R	S	F	A	S	E	A	V	R	I	G	T	E	G	S	P	V	85		
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Db 492 ----- 491
QY 747 ALRREDFPVHVDHTAGGLATYFAAAQAGADAVDGASAPLSGTTSPSLSAIVAFA 806
Db 492 ----- 491
QY 807 HTRDRTGLSLEAVSDLEPYWEAVRGVLYLPFESGTPGTGRVYRHEIPGGQLSNLRAQATA 866
Db 492 ----- 491
QY 867 LGLADRFELIEDNAAVNEMLGRP-TKVTPESSKVVGDALHLVAGVDPADPAADPQKYD 925
Db 492 ----- 491
QY 926 IPDSVIAFLRGLGPNPGWPEPLRTRALEGRSEKAPLITEVPEEQAHLDADDKSKERN 985
Db 518 ----- 517
QY 986 SLNRLFPKPTPEFLERRRFNGNTSALDDREFYGLVEGETLIRLPDVRTPLVRLDAI 1045
Db 518 ----- 517
QY 1046 SEPDDK-GMRNVVANVGOLRPMRVDRSVESVTATAEKADSSNKGHVAAPAGV-VTVT 1103
Db 572 GDLNKKTGREVDFLNGEMKIRVADRQKQVETVTKSRADMDHDPHIGAPMAGVIVEVK 631
QY 1104 VAEDEVKAGDAVAIIEAMKMEATITASVDGKIERYVVPAAATKVEGGDLIVV 1156
Db 632 VHKGLIKKQPVAVLSAMKMEMIISPSDQGVKEVFSVDGENVDSLLVLL 684

RESULT 7

US-09-634-238-276
; Sequence 276, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Kavukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE REFERENCE: 11000.1043U1
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 276
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-276

Query Match 18.5%; Score 1084; DB 4; Length 456;
Best Local Similarity 51.3%; Pred. No. 1.6e-77;
Matches 230; Conservative 66; Mismatches 142; Indels 10; Gaps 7;

QY 224 VYVERAVINQHIEVQILGDRGVEVHLVDRCSLQRRHQKVEIAPAHLDPELRDRIC 283
Db 12 MYVEKTIASAKHVEQVLDGHEHLHLFERDCSVORROOKVVEIAPAVLALNRIC 71
QY 284 ADAVKCRSIGVQAGATVFLVDEKGNHVFIEANPRIOVEHVTEVTEVDLVKQMRLA 343
Db 72 QSAVDLMASHVENAGTVEFLVD-GDQYFIEVNPVQVEHTEITLITGDVIVQSOLRIA 130
QY 344 AGATL-KELGL-TQDKIKHGAALQCRITTEDPNNGFRPDGTGTITAYRSPGGAGVRLD-G 400

Db 131 AGADLEADLHLPOODALRENGAAIQCRITTEDPENNFMPTGTINTYRSPGGFIRLDVG 190
QY 401 AALGGEITAHFDSMLVKMTCRSGDETAVARAQRALAEETVSGVATINTIGFLRALLREED 460
Db 191 NAYAGAVSPYFDSLLVKSASVHAPSPAAVAKMQRALHEFQITGVTKTNVAFLEHLLATQT 250
QY 461 FTSKRIATGFIGDHPHLLQAPPADDEQGRILDYADVTYVKNKPHGV-RPKDVAAPIDKLPN 519
Db 251 FRTGEAETAFIDAHPELLQVQAKPDIASRLLSWISDVTVNGFKGVERQSQKYP--ELQY 308
QY 520 IKDLPFPRGSRD---RLKQLGPAFAFARDLREQDALAVTDTTFRDAHQSLLATVRSFALK 576
Db 309 TRFAAAKPTQDLVALLKNEGAQAVTDWKAHPALLITDITFRDAHQSLFATMRTRDML 368
QY 577 PRAEAVAKLTPELLSVYEWGGAITYDVAMRFLPEDPMDRLDELREAMPNVNIQMLLRNT 636
Db 369 TVAEDMGNGLNPLNFSMEVWGGATFDVAYRFLNEDPWRLKLRALPHLLQLMFRGSA 428
QY 637 VGYTPYDSCVAFVKEAASSGVDFIRI 664
Db 429 VGYQNPDPNVIKAFINQAAANDGVDFIRI 456

RESULT 8

US-09-433-043B-122
; Sequence 122, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-433-043B-122

Query Match 17.7%; Score 1039.5; DB 4; Length 593;
Best Local Similarity 44.3%; Pred. No. 8.4e-74;
Matches 229; Conservative 80; Mismatches 177; Indels 31; Gaps 6;

QY 29 FKKILVANRGEJAVRAAFRAALLETGAATVAIYPREDRGSFHRSPFASAVRIGTSGSPVKAY 88
Db 3 FDKILLANRGEJALRILRACEEMGIATIAVHSTVDNRNALHVLQADAVCIG-EPASAKSY 61
QY 89 LDIDEIIGAARKVKADAIYPGYGFLSENAQLARECAENGITITGPTPEVLDLTGDKSRV 148
Db 62 LNIPIIAAALTRNASAIHPGYGFLSENAKFAEICADHHAIFGTPPEAIRLMGDKSTAK 121
QY 149 TAAKAGLPIVAES-----TPSKNIDDDIVKSAGQTYPIFVKAAGGGGRMRFVSSPDE 203
Db 122 ETMQKAGVTPVPGSEGLVETEQEGLE---LAKDIGYPVMIKATAGGGGRMLRVRSPDE 177
QY 204 LRKATEASREAAFAFGDGSVYVERAVINPQHIEVQILGDRGVEVHLVDRCSLQRRHQ 263
Db 178 FVKLFLAAGEAGAGAGNAGVYIEKFIERPRHIEFQILADNIGNVHLGERDCSLQRRNQ 237
QY 264 KYVEIAPAHLDPELRDRICADAVKFCRSIGYQAGATVEFLVDEKGNHVFIEANPRIOVE 323
Db 238 KLEEAAPSALDRLREKMGQAQVAAQFINTYAGATTIEFLDRSGQFFVEMENRQIVE 297


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; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-422-560A-6

Query Match          17.6%  Score 1032.5; DB 2; Length 447;
Best Local Similarity 48.2%; Pred. No. 1.9e-73;
Matches 216; Conservative 71; Mismatches 148; Indels 13; Gaps 4;

QY 29 FKILVANRGEIAVRAFAALETGAATVAIYPREDGRSFHRSFASAVRIGTEGSPVKAY 88
Db 3 FDKILIANRGEIALRILRACEEMGIATIAVHSTVDNRNALHVQLADEAVCIG-EPASAKSY 61

QY 89 LDDEIITGAACKVKADAIYPGYFLSNAQALRECAENGITFTGPTPEVLDLTGDKSRAY 148
Db 62 LNPITIAAALTRNASAIHPGYFLSNAKFAEICADHIAFIPTPEAIRLMDGDKSTAK 121

QY 149 TAAKKAGLPVLAES-----TPSKNIDDIVKSAGQTYPIEVKAVAGGGGRMRFVSPDE 203
Db 122 ETQKAGVPTVPSEGLVETEQEGLE---LAKDIGYPMVKATAGGGGRMRLVRSPE 177

QY 204 LRKLATEASREAAAFDGGVYVERAVINPQHIEVQLIGDRTGEVHLYERDCSLORRHQ 263
Db 178 FVKFLAAQGEAGAAFGNAGVYIEKFTERPHEIFQILADNYGNVHILGERDCSIQRNQ 237

QY 264 KVEIAPAQHLDPRLDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVTIEMNPRIQVE 323
Db 238 KLEEAPSPALDSDLREKMQAAVKAQFNYTGAGTIEFLDLSGGQFYEMNTRIQVE 297

QY 324 HTVTEEVTEVDLVKAQMRLAAGATLKEGLTQDKIKTHGAALOCRTITDPNNGFRPDTG 383
Db 298 HPVTMTGVDLLVEQIRIAGGERLR---LTQDQVVLRGHAIECRINAEDPDHDFRPAPG 354

QY 384 TITAYRSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTVS 443
Db 355 RISGLPPGGVGRIDSHVTDYQIPPYDLSLGLKLVWGPDRATAINRMKRALRECAIT 414

QY 444 GVATNIGLRALLREEDFTSKRIATGFI 471
Db 415 GLPTTIGFHQRIMENPQFLOGNVSTSFV 442

RESULT 11
US-08-468-793-6
; Sequence 6, Application US/08468793
; Patent No. 6177267
; GENERAL INFORMATION:
; APPLICANT: Haseikorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
; METHODS OF USE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,793
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/422,560
; FILING DATE: 14-APR-1995
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; CLASSIFICATION: 800
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; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/611,107
; APPLICATION NUMBER: US/08/611,107
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/09340
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 08/422,560
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-611-107-8

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Query Match 17.1%; Score 1005.5; DB 1; Length 453;
Best Local Similarity 47.1%; Pred. NO. 2.7e-71;
Matches 209; Conservative 72; Mismatches 158; Indels 5; Gaps 3;

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QY 29 FKKILVANGETAVRAALETGAATVAIYPREDRGSPHRSFASAVRIGTEGSPVKAY 88
DB 3 FKKILVANGETAVRAALETGAATVAIYPREDRGSPHRSFASAVRIGTEGSPVKAY 88
QY 89 LDIDEIIGAIAKVKADAIYPGYGFLSENALRECAENGITFTGPTPEVLDLTGDKSRV 148
DB 62 LNPINIAAALTRNNAIHPGYGFLSENALRECAENGITFTGPTPEVLDLTGDKSRV 148
QY 149 TAAKAGLPVLAESTP-SKNIDDIKVSAGQTYPIFVKAVAGGGRGMRVSPDELRL 207
DB 122 ETMQRVGVPTIPSGDGLTDDVSAKVAEIGYPVMKATAGGGGRGMRVSPDELRL 207
QY 208 ATEASREAAFGDGSVYVERAVINPQHLVEQILGDRTEGVVHLVYERDCSLORRHQVVE 267
DB 182 FLAAGEAEEAAGNPGLYLEKFDPRHVEFQILADAYGNVHLGERDCSLORRHQVVE 267
QY 268 IAPQHLDELDRICADAVKFCRSIGYOGAGTVEFLVDEKHNHVFIEIENPRIQVHTVT 327
DB 242 EAPSPALSADLRQKMGDAVKAQVAGYIGAGTVEFLVDEKHNHVFIEIENPRIQVHTVT 327
QY 328 EEVTEVDLVKAQMLAAGATLKGELGTQDKIKTHGAALOCRTTDPNNGFRPDTGTITA 387
DB 359 YLPPGGPGVRVDSHVYDVEIPYDLSLIGKLVWGATREALARMQALRECAITGLPT 418
QY 448 NGIFLALLREDFTSKRTATGEI 471
DB 419 TLSFHQLMLQMPFELRGELYTNFV 442

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RESULT 13

```

US-08-422-560A-8
; Sequence 8, Application US/08422560A
; Patent No. 5910626
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
; TITLE OF INVENTION: METHODS FOR USE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,560A
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/956,700
; FILING DATE: 02-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:152/WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-422-560A-8

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Query Match 17.1%; Score 1005.5; DB 2; Length 453;
Best Local Similarity 47.1%; Pred. NO. 2.7e-71;
Matches 209; Conservative 72; Mismatches 158; Indels 5; Gaps 3;
QY 29 FKKILVANGETAVRAALETGAATVAIYPREDRGSPHRSFASAVRIGTEGSPVKAY 88
DB 3 FKKILVANGETAVRAALETGAATVAIYPREDRGSPHRSFASAVRIGTEGSPVKAY 88
QY 89 LDIDEIIGAIAKVKADAIYPGYGFLSENALRECAENGITFTGPTPEVLDLTGDKSRV 148
DB 62 LNPINIAAALTRNNAIHPGYGFLSENALRECAENGITFTGPTPEVLDLTGDKSRV 148
QY 149 TAAKAGLPVLAESTP-SKNIDDIKVSAGQTYPIFVKAVAGGGRGMRVSPDELRL 207
DB 122 ETMQRVGVPTIPSGDGLTDDVSAKVAEIGYPVMKATAGGGGRGMRVSPDELRL 207
QY 208 ATEASREAAFGDGSVYVERAVINPQHLVEQILGDRTEGVVHLVYERDCSLORRHQVVE 267
DB 182 FLAAGEAEEAAGNPGLYLEKFDPRHVEFQILADAYGNVHLGERDCSLORRHQVVE 267
QY 268 IAPQHLDELDRICADAVKFCRSIGYOGAGTVEFLVDEKHNHVFIEIENPRIQVHTVT 327
DB 242 EAPSPALSADLRQKMGDAVKAQVAGYIGAGTVEFLVDEKHNHVFIEIENPRIQVHTVT 327
QY 328 EEVTEVDLVKAQMLAAGATLKGELGTQDKIKTHGAALOCRTTDPNNGFRPDTGTITA 387
DB 302 EMITGLDLIAEQIRIAQGEALR---FRQADIQLRGAIECRINAEDPEYNFRPNRGRITG 358
QY 388 YRSPGGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTVSGVAT 447

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Db      359 YLPPGGVGVVDHSHVYTDYEIPPYDSLIGKLIWGAIRREEARQALRECAITGLPT 418
QY      448 NIGFLRALIREDEFTSKRIATGFI 471
Db      419 TLSFHQLMOWPEFLRGELYTNFV 442

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RESULT 14
 US-08-468-793-8
 ; Sequence 8, Application US/08458793
 ; Patent No. 6177267
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselkorn, Robert
 ; APPLICANT: Gornicki, Piotr
 ; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS OF USE
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: United States of America
 ; ZIP: 77210

Query Match	17.1%	Score 1005.5;	DB 3;	Length 453;
Best Local Similarity	47.1%	Pred. No. 2.7e-71;		
Matches 209;	Conservative 72;	Mismatches 158;	Indels 5;	Gaps 3;
QY	29	FKKILVNRGEIAVRAFAALETGAATVAIYPREDRGSHFRSFASEAVRIGTEGSPVKAY	88	
Db	3	FNKILVNRGEIALRIILTCETELGIGTIAVSHSVDRNALHVLQLEADAVCIG-EARSSKSY	61	
QY	89	LDEIDTGAKKVKADAIYGYGFLSENQAOLARECAENGITTTGTPTEVLDTGDKSRAY	148	
Db	62	LNIPNIAAALTRNASAIHPGYGFLAENRFAEICADHLLTIGTSPDSIRAMGDKSTAK	121	
QY	149	TAANKAGIPVLAESTP-SKNIDDIIVSAEQTIPIYFKVAGVGGRGMRFTVSSPDELKRL	207	

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122 ETMORVGVTIPGSDGLTLDVDSAAKVAEEIGYPVMIKATAGGGKGMRLVREPADLEKL 181
208 ATEASREAAAFDCGSVYVERAVINPOHIEVOILGDRTEGVVHLVERDCSLORRHOKVVE 267
182 FLAQQGEAAAFNGFLYLEFIDRPHRVEFOILADAGNVVHLGERDCSIORRQKLE 241
268 IAPAQHLDPDLRDRICADAVKFCRSIGYGAGTVEFLVDEKGNHVFIEMNPRIOVEHTVT 327
242 EAPSPALSADLRQKMGDAVKVAQIAGYIGACTVEFLVDATGCTFYFEMENRIOVEHPVT 301
328 BEVTEVDLVKAOMRLAAGATLKEGLTODKTIKTHGAALQCRUITTEDPNNGFRPDGTIFA 387
302 EMITGLDIIARQIRIAQGEALR---FRQADIQLRGHATECRINAEDPEYFNRPNEGRI 358
388 YRSPGGAGVRLDGAALQGETTAHEDSMLVKMTCHGSDFEFATAVARAQALAEFTVSGVAT 447
359 YLPPGFGVRVDVSHVYTDYEPYDLSLIGKLIWVGATREAIARMQALRECAITGLPT 418
448 NIGFRLALLREEDFTSKRIATGFI 471
419 TLSFHQIMLQMPFLRGELYTNFV 442

RESULT 15
US-09-433-043B-121
: Sequence 121, Application US/09433043B
: Patent No. 6399342
: GENERAL INFORMATION:
: APPLICANT: HASELKORN, ROBERT
: APPLICANT: GORNICKI, PIOTR

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RESULT 15
US-09-433-043B-121
; Sequence 121, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:33875
; CURRENT APPLICATION NUMBER: US/09/433,043B
; CURRENT FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 121
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-121

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Query Match	17.1%;	Score 1003.5;	DB 4;	Length 453;
Best Local Similarity	47.1%;	Pred. No. 3.9e-71;		
Matches 209;	Conservative	72;	Mismatches 158;	Indels 5; Gaps 3;

QY	29	FKKILVANRGEIAVRAFRRAALETGAAITVAIYIPREDRGSFHRSEAFSEAVRIGTSGPVKAY	88
Db	3	FNKILIANRGEIALRIILRTCEEIGIGITIAVHSTVDRNALHVLQLEADAEVCIIG-EEASSKSY	61
QY	89	LDIDEIIGAARKVKKADAIYPCYGFLSNAQLARECAENGITFIPTPEVLDLTGDKSPAV	148
Db	62	LNIPNIIAAALTNRNAAIHPGYGFLEARNARFAEICADHHLTFIIPGSPDSTRAMGDGKSTAK	121
QY	149	TAAKKAGLPLVALESTP-SKNIDIDIVKSAEGOTYPIFYKAVAGGGGRGMRFYSSPDELKRL	207
Db	122	ETMQRVGVPIPCSDGLLTTVDSSAAKVAALIGYPMIKATAGGGGRGMRILVREPADLEKL	181
QY	208	ATEASREAEAAFGDGSVYVERAVINPQHIEVQILGDRGTGEVHLYEDCSLQRHQRKWE	267
Db	182	FLAAQGEAEAAFCNPGILYEKFTDRPRHVESQILADAYGNVVLHGEDRDCSTQRHQLLE	241
QY	268	IAPAQHLDELDRDICADAVKFCRSTGYGAGNVFEFLVDEKGNHVFTEMPRIQVEHTVT	327
Db	242	EAPSPALSDLRKMGSDAALVKVQAQYIGAGTVEFLVDATGNFYFMEMTRIOVEHPVT	301

GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
4760.992 Million cell updates/sec

Title: US-09-974-973A-2

Perfect score: 5865

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Scoring table: BLOSUM62

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Searched: 566894 seqs, 151307093 residues

Total number of hits satisfying chosen parameters: 566894

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*

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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5865	100.0	1157	10 US-09-974-973-4	Sequence 4, Appli
3	5759	98.2	1140	10 US-09-974-973-19	Sequence 19, Appli
4	5759	98.2	1140	10 US-09-738-626-4265	Sequence 4265, Ap
5	5759	98.2	1140	15 US-10-045-072-2	Sequence 2, Appli
6	2489	42.4	1147	9 US-09-815-242-5468	Sequence 5468, Ap
7	2460.5	42.0	1142	9 US-09-815-242-10806	Sequence 10806, A
8	2300	39.2	1073	9 US-09-815-242-12361	Sequence 12361, A
9	1032.5	17.6	447	9 US-09-767-479-6	Sequence 6, Appli
10	1005.5	17.1	453	9 US-09-767-479-8	Sequence 8, Appli
11	979.5	16.7	471	9 US-09-815-242-5215	Sequence 5215, Ap
12	956	16.3	449	9 US-09-815-242-13885	Sequence 13885, A
13	950	16.2	448	9 US-09-815-242-11160	Sequence 11160, A
14	941	16.0	1171	15 US-10-156-761-14226	Sequence 14226, A
15	940	16.0	449	9 US-09-815-242-10330	Sequence 10330, A

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16 936.5 16.0 455 9 US-09-815-242-13617 Sequence 13617, A
17 935.5 16.0 455 9 US-09-815-242-13364 Sequence 13364, A
18 921 15.7 449 9 US-09-815-242-12063 Sequence 12063, A
19 919 15.7 458 9 US-09-815-242-11321 Sequence 11321, A
20 912 15.5 590 15 US-10-156-761-10874 Sequence 10874, A
21 909 15.5 443 9 US-09-815-242-4963 Sequence 4963, Ap
22 909 15.5 456 9 US-09-815-242-10924 Sequence 10924, A
23 906 15.4 590 12 US-10-045-612A-25 Sequence 25, Appli
24 902 15.4 455 9 US-09-815-242-11558 Sequence 11558, A
25 897 15.3 725 15 US-10-160-501-17 Sequence 17, Appli
26 896 15.3 725 15 US-10-224-539A-2 Sequence 2, Appli
27 896 15.3 725 15 US-10-224-539A-9 Sequence 9, Appli
28 893 15.2 590 12 US-10-045-612A-26 Sequence 26, Appli
29 890 15.2 700 15 US-10-156-761-12811 Sequence 12811, A
30 880.5 15.0 591 10 US-09-738-626-6940 Sequence 6940, Ap
31 856.5 14.6 446 9 US-09-815-242-5418 Sequence 5418, Ap
32 856.5 14.6 453 9 US-09-815-242-12562 Sequence 12562, A
33 837 14.3 448 9 US-09-815-242-5806 Sequence 5806, Ap
34 834 14.2 451 9 US-09-815-242-13127 Sequence 13127, A
35 829.5 14.1 616 15 US-10-156-761-11400 Sequence 11400, A
36 653 11.1 464 15 US-10-169-048-28 Sequence 28, Appli
37 633 10.8 358 9 US-09-815-242-12939 Sequence 12939, A
38 583.5 9.9 2257 9 US-09-767-479-10 Sequence 10, Appli
39 533.5 9.1 2257 12 US-09-839-477-8 Sequence 8, Appli
40 437.5 7.5 483 15 US-10-083-357-1328 Sequence 1328, Ap
41 423.5 7.2 262 15 US-10-224-539A-5 Sequence 5, Appli
42 377.5 6.4 158 9 US-09-815-242-5031 Sequence 5031, Ap
43 300.5 5.1 163 10 US-09-895-913A-324 Sequence 324, Ap
44 252 4.3 1073 16 US-10-210-115-20 Sequence 20, Appli
45 251 4.3 124 9 US-09-205-658-240 Sequence 240, App

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ALIGNMENTS

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RESULT 1
US-09-974-973-2
; Sequence 2, Application US/09974973
; Patent No. US20020177202A1
; GENERAL INFORMATION:
; APPLICANT: Hanke, Paul D.
; TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacter
; FILE REFERENCE: 1533.1230001/MAC/RGM
; CURRENT APPLICATION NUMBER: US/09/974, 973
; CURRENT FILING DATE: 2001-10-21
; PRIOR APPLICATION NUMBER: US 60/239, 913
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1157
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-974-973-2

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Query Match 100.0%; Score 5865; DB 10; Length 1157;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTAITLGGLLKGIITLVSTHTSTLPAPFKKILVANRGEIAVRAFRALLETGAATVAIYP 60
Db 1 MTAITLGGLLKGIITLVSTHTSTLPAPFKKILVANRGEIAVRAFRALLETGAATVAIYP 60
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Db 61 REDRGSFHRFSFASEAVRIGTEGSPVKAYLIDIEIGAAKKVKADAIYPGVGFLSENAQLA 120
QY 121 RECAENGITFIGTPEVLDTGDKSRAYTAACKAGLPVLAESTPFSKNIDDIKVASGQTY 180
Db 121 RECAENGITFIGTPEVLDTGDKSRAYTAACKAGLPVLAESTPFSKNIDDIKVASGQTY 180
QY 181 PIFKAVAGGGGRGMFVSSPDRLKATEASREAAAFDGGSVYVERAVINPQHLEVTQI 240
Db 181 PIFKAVAGGGGRGMFVSSPDRLKATEASREAAAFDGGSVYVERAVINPQHLEVTQI 240

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Db 181 PIFKAVAGGGGGRMFVSSPDELRLKLAETASREAAAFGDSGVYVERAVINPQHIEVQI 240
QY 241 LGDRTGEVHLXERDCSLORRHOKVVEIAPQAHLDPDLDRICADAVKFCRSIGYOGAGT 300
Db 241 LGDRTGEVHLXERDCSLORRHOKVVEIAPQAHLDPDLDRICADAVKFCRSIGYOGAGT 300
QY 301 VEEFLVDEKGNHVFIEKNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKBELGTLQDKIKT 360
Db 301 VEEFLVDEKGNHVFIEKNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKBELGTLQDKIKT 360
QY 361 HGAALQCRITTEDPNNGFRPDTGTITAYRSPGAGVRLDGAALGGEITAHFDSMLVKMT 420
Db 361 HGAALQCRITTEDPNNGFRPDTGTITAYRSPGAGVRLDGAALGGEITAHFDSMLVKMT 420
QY 421 CRGSDFTAVARAQALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQA 480
Db 421 CRGSDFTAVARAQALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQA 480
QY 481 PPADDEQGRILDYADVTVNKPHGVKPKVAAPIDKLPNTKOLPLPRGSRDLKQLGPAA 540
Db 481 PPADDEQGRILDYADVTVNKPHGVKPKVAAPIDKLPNTKOLPLPRGSRDLKQLGPAA 540
QY 541 FARDLEQDALAVTDTTFRDAHOSLLATRVRSFALKPAEAVAKLTPELLSVEAWGATY 600
Db 541 FARDLEQDALAVTDTTFRDAHOSLLATRVRSFALKPAEAVAKLTPELLSVEAWGATY 600
QY 601 DVAMRFLFEDPWRDLDELREAMPNVNIQMLLRGNVTGYTPYPSVCRAFVKEAASSGVD 660
Db 601 DVAMRFLFEDPWRDLDELREAMPNVNIQMLLRGNVTGYTPYPSVCRAFVKEAASSGVD 660
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QY 721 KSGAHILAIKDMAGLLRPAAVTKLVTALRREFDLPVHVHTDAGGOLATYFAAAQAGAD 780
Db 721 KSGAHILAIKDMAGLLRPAAVTKLVTALRREFDLPVHVHTDAGGOLATYFAAAQAGAD 780
QY 781 AVDGASAPLSGTTSQPSLSAIVAFAAFAHTRDRTGLSLEAVSDLEPVEAVRGLYLPESGT 840
Db 781 AVDGASAPLSGTTSQPSLSAIVAFAAFAHTRDRTGLSLEAVSDLEPVEAVRGLYLPESGT 840
QY 841 PGPTGRVYRHEIFGGQISNLRQAATLGLADRELIEDNTAAVNEMLGRPTKVTPSSKV 900
Db 841 PGPTGRVYRHEIFGGQISNLRQAATLGLADRELIEDNTAAVNEMLGRPTKVTPSSKV 900
QY 901 GDALHLVAGVDPADPAADPKYDIPDSVIAFLRGELGNPPGWPPEPLTRALEGRSEG 960
Db 901 GDALHLVAGVDPADPAADPKYDIPDSVIAFLRGELGNPPGWPPEPLTRALEGRSEG 960
QY 961 KAPLTVPEEEOAHLDAADSKERRNSLNRLFFPKPTPEEFLEHRRRFGNTSALDDREFY 1020
Db 961 KAPLTVPEEEOAHLDAADSKERRNSLNRLFFPKPTPEEFLEHRRRFGNTSALDDREFY 1020
QY 1021 LVGREGTILRLPVRTPLLYRLDAISPPDKGRNVVANNVNGOIRPMRVDRDSVESVAT 1080
Db 1021 LVGREGTILRLPVRTPLLYRLDAISPPDKGRNVVANNVNGOIRPMRVDRDSVESVAT 1080
QY 1081 AERADSSNKGHVAAPFAGVVTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIERYV 1140
Db 1081 AERADSSNKGHVAAPFAGVVTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIERYV 1140
QY 1141 VPAATKVEGDLIVVVS 1157
Db 1141 VPAATKVEGDLIVVVS 1157

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RESULT 2

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US-09-974-973-4
; Sequence 4, Application 05/09974973
; Patent No. US20020177202A1
; GENERAL INFORMATION:
; APPLICANT: Hanke, Paul D.

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; TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacter
; FILE REFERENCE: 1533.1230001/MAC/RGM
; CURRENT APPLICATION NUMBER: US/09/974, 973
; CURRENT FILING DATE: 2001-10-21
; PRIOR APPLICATION NUMBER: US 60/239, 913
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1157
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-974-973-4

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Query Match 100.0%; Score 5865; DB 10; Length 1157;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MTAITLGGLLKGIIITLVSTHTSTLPAFKKILVANRGEIATVRAALETGAATVAIYP 60
Db 1 MTAITLGGLLKGIIITLVSTHTSTLPAFKKILVANRGEIATVRAALETGAATVAIYP 60
QY 61 REDGSGFHRSFASFAVRIGTEGSPVKAYLDIDELIGAKKVKADAIYPGYGFLSENAQLA 120
Db 61 REDGSGFHRSFASFAVRIGTEGSPVKAYLDIDELIGAKKVKADAIYPGYGFLSENAQLA 120
QY 121 RECAENGITFIGTPEVILDTGDKRAVTAAKKAGLPVLAESTPSKNIDDIVKSAEGQTY 180
Db 121 RECAENGITFIGTPEVILDTGDKRAVTAAKKAGLPVLAESTPSKNIDDIVKSAEGQTY 180
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Db 181 PIFKAVAGGGGGRMFVSSPDELRLKLAETASREAAAFGDSGVYVERAVINPQHIEVQI 240
QY 241 LGDRTGEVHLXERDCSLORRHOKVVEIAPQAHLDPDLDRICADAVKFCRSIGYOGAGT 300
Db 241 LGDRTGEVHLXERDCSLORRHOKVVEIAPQAHLDPDLDRICADAVKFCRSIGYOGAGT 300
QY 301 VEEFLVDEKGNHVFIEKNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKBELGTLQDKIKT 360
Db 301 VEEFLVDEKGNHVFIEKNPRIQVEHTVTEEVTEVDLVKAQMRLAAGATLKBELGTLQDKIKT 360
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Db 541 FARDLEQDALAVTDTTFRDAHOSLLATRVRSFALKPAEAVAKLTPELLSVEAWGATY 600
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Db 781 AVDGASAPLSGTTSQPSLSAIVAFAAFAHTRDRTGLSLEAVSDLEPVEAVRGLYLPESGT 840

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QY 841 PGPTGRVYRHEIPGQSLNRAQATAGLADREFELIEDNYAAVNEMLGRPTKVTSSKVV 900
 DB 841 PGPTGRVYRHEIPGQSLNRAQATAGLADREFELIEDNYAAVNEMLGRPTKVTSSKVV 900
 QY 901 GDALHLVYAGVDPADFAADPKQYDIPDSVIAFLRGELGNPPGGWPELRTALRSESEG 960
 DB 901 GDALHLVYAGVDPADFAADPKQYDIPDSVIAFLRGELGNPPGGWPELRTALRSESEG 960
 QY 961 KAPLITEVEEQAHLDADDSKERRNSLNRLFPKPTTEFLEHRRRFGNTSALDDREFFYG 1020
 DB 961 KAPLITEVEEQAHLDADDSKERRNSLNRLFPKPTTEFLEHRRRFGNTSALDDREFFYG 1020
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 QY 1081 AEKADSSNKGHVAAFPAGVVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERYV 1140
 DB 1081 AEKADSSNKGHVAAFPAGVVTVAEGDEVKAGDAVAIIEAMKMEATITASVDGKIERYV 1140
 QY 1141 VPAATKVEGGDLIVVVS 1157
 DB 1141 VPAATKVEGGDLIVVVS 1157

RESULT 3
 US-09-974-973-19
 ; Sequence 19, Application US/09974973
 ; Patent No. US20020177202A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hanke, Paul D.
 ; TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from *Corynebacterium*
 ; FILE REFERENCE: 1533 1230001/MAC/RGM
 ; CURRENT APPLICATION NUMBER: US/09/974,973
 ; CURRENT FILING DATE: 2001-10-21
 ; PRIOR APPLICATION NUMBER: US 60/239,913
 ; PRIOR FILING DATE: 2000-10-13
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 19
 ; LENGTH: 1140
 ; TYPE: PRT
 ; ORGANISM: *Corynebacterium glutamicum*
 US-09-974-973-19

Query Match 98.2%; Score 5759; DB 10; Length 1140;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1133; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 18 VSTHTSSTLPAPKILVANRGEIAYRAFAALETGAATVAIYPREDRGSFHRSEAFSEAVR 77
 DB 1 MSTHTSSTLPAPKILVANRGEIAYRAFAALETGAATVAIYPREDRGSFHRSEAFSEAVR 60
 QY 78 IGTEGSPKAYLIDIDEITGAKKVADAIYPGYGFSENAQLARECAENGITFIPTPEV 137
 DB 61 IGTEGSPKAYLIDIDEITGAKKVADAIYPGYGFSENAQLARECAENGITFIPTPEV 120
 QY 138 LDLTGDKSRVTAANKAGLPVLAESTPSKNIDDIIVKSAGQYPIFVKAVAGGGGRMRF 197
 DB 121 LDLTGDKSRVTAANKAGLPVLAESTPSKNIDDIIVKSAGQYPIFVKAVAGGGGRMRF 180
 QY 198 VSSPDLRLKLAETASREAAFGDGVYVERAVINPQHIEVQILGDRGTGEVHLHERDCS 257
 DB 181 VASPDRLKLAETASREAAFGDGVYVERAVINPQHIEVQILGDRGTGEVHLHERDCS 240
 QY 258 LQRRHQKVEIAPAHLDPELDRICADAVKFCRSIGYGAGTVEFLVDEKGNHVFIEMN 317
 DB 241 LQRRHQKVEIAPAHLDPELDRICADAVKFCRSIGYGAGTVEFLVDEKGNHVFIEMN 300
 QY 318 PRIQVEHTVTEEVTEVDLVKAQMLRAAGATLKGTLQDKIKTHGAAQCRIITTEDPNNG 377
 DB 301 PRIQVEHTVTEEVTEVDLVKAQMLRAAGATLKGTLQDKIKTHGAAQCRIITTEDPNNG 360

QY 378 FRPDTGTTAYRSPGAGVRLDGAALGGEITTAHFDSMLVKMTCRGSDFETAVARAQAL 437
 DB 361 FRPDTGTTAYRSPGAGVRLDGAALGGEITTAHFDSMLVKMTCRGSDFETAVARAQAL 420
 QY 438 AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDDQGRILYDLADV 497
 DB 421 AEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDDQGRILYDLADV 480
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 DB 481 TVNKHGVRPKDVAAPIDKLPNIKDLPLPRGSRDLKOLGPAFAAFARDLREQDALAVDTPT 540
 QY 558 FDAHQSLATVRSFALKPAEAETAKLTPELLSVEANGGATYDVAMRFLFEDPDWDLDE 617
 DB 541 FDAHQSLATVRSFALKPAEAETAKLTPELLSVEANGGATYDVAMRFLFEDPDWDLDE 600
 QY 618 LREAMPNVNIQMLLRGRNTVGYTPYDPSVCRAVFAVKEAASSGVDFRIFDALNDVSMRPA 677
 DB 601 LREAMPNVNIQMLLRGRNTVGYTPYDPSVCRAVFAVKEAASSGVDFRIFDALNDVSMRPA 660
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 DB 661 IDAVLETNTVAEVAAMAYSGDLSDPNEKLYTLDYILKMAEETVKSGAHLAIKDMAGLLR 720
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 DB 721 PAAVTKLVTALRREFDLPVHVHTHDTAGGQLATYFAAAQAGADAVDASAPLSGTTSPS 780
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 DB 781 LSAIVAAFAHTRDRDTGLSLEAVSDLEPYWEAVRGLYLPFESCTPGTGRVYRHEIPGGQL 840
 QY 858 SNLRAQATAGLADREFELIEDNYAAVNEMLGRPTKVTSSKVVGDALHLVAGVDPADF 917
 DB 841 SNLRAQATAGLADREFELIEDNYAAVNEMLGRPTKVTSSKVVGDALHLVAGVDPADF 900
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 DB 961 DDSKERRNSLNRLFPKPTTEFLEHRRRFGNTSALDDREFFYGLVEGRETILRLPDVTRP 1020
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 DB 1081 GYVTVTVAGDEVKAGDAVAIIEAMKMEATITASVDGKIERYVVPAAATKVEGGDLIVVVS 1140

RESULT 4
 US-09-738-626-4265
 ; Sequence 4265, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; CURRENT FILING DATE: 2000-12-18

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; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4265
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4265

Query Match          98.2%; Score 5759; DB 10; Length 1140;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1133; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 18 VSTHTSSTLPAPKKILVANRGEIATVAFRAALAEATGATVIAIYPREDRGSFHRSEAVR 77
Db 1 MSTHTSSTLPAPKKILVANRGEIATVAFRAALAEATGATVIAIYPREDRGSFHRSEAVR 60

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Db 61 IGTEGSPVKAYLDDIIEIGAAKKVADAIYPGYGFLSENAQLARECAENGIITGPTPEV 120

QY 138 LDTGDKSRVTAATAKAGLVLAESTPSKNIDIVKSAEGQTYPIEVKAVAGGGGRMRF 197
Db 121 LDTGDKSRVTAATAKAGLVLAESTPSKNIDIVKSAEGQTYPIEVKAVAGGGGRMRF 180

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Db 181 VASPEDELKRLATASREAEAFDGGVYVERAVINPQHIEVQLIGDRTGEVHLVERDCS 240

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Db 241 LQRRHQKVVEIAPAQHLDPDLRDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIE 300

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Db 361 FRPDGTGIIATYRSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFETAVARAQ 420

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Db 421 AEFTVSGVATNIGFLRALLREEDFTSKRIATGATGFIADPHLLQAPPADDEQGRILDY 480

QY 498 TVNKPVGVRPKDVAAPIDKLPNIKDLPLPGSRDLKQLGPAFAFARLDREQDALAV 557
Db 481 TVNKPVGVRPKDVAAPIDKLPNIKDLPLPGSRDLKQLGPAFAFARLDREQDALAV 540

QY 558 FRDAHQSLLATVRSFALPAAEAVAKLPELLSVEAWGATVDVAMRFLFEDPWRDLDE 617
Db 541 FRDAHQSLLATVRSFALPAAEAVAKLPELLSVEAWGATVDVAMRFLFEDPWRDLDE 600

QY 618 LREAMPNVIQMLRGRTVGTPTYPDSVCRAVKEAASGGVDIFRIFDALNDVSMRPA 677
Db 601 LREAMPNVIQMLRGRTVGTPTYPDSVCRAVKEAASGGVDIFRIFDALNDVSMRPA 660

QY 678 IDAVLENTAVAEVAMAYSGDSLDPNEKLYTLDYILKMAEIEIVKSAHILAKDMAGLL 737
Db 661 IDAVLENTAVAEVAMAYSGDSLDPNEKLYTLDYILKMAEIEIVKSAHILAKDMAGLL 720

QY 738 PAAVTKLVTLALREFDLPVHVHTHTAGGOLATYFAAQAQADAVDGCASAPLSGITSQ 797
Db 721 PAAVTKLVTLALREFDLPVHVHTHTAGGOLATYFAAQAQADAVDGCASAPLSGITSQ 780

QY 798 LSAIVAAFAHTRDRTGLSLEAVSDLEPYWEAVRGILYLPESGTPGPTGVRVHEIPGG 857
Db 781 LSAIVAAFAHTRDRTGLSLEAVSDLEPYWEAVRGILYLPESGTPGPTGVRVHEIPGG 840

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QY 858 SNLRAQATATLGLADRFELIEDNYAAVNMELGRPTKVTSSKVVGDIALHLWAGVDPAD 917
Db 841 SNLRAQATATLGLADRFELIEDNYAAVNMELGRPTKVTSSKVVGDIALHLWAGVDPAD 900

QY 918 AADPQKYDIPDSVIAFLRGEIAGNPPGGWPEFLRTRALEGRSEKAPLTEVPEEQAH 977
Db 901 AADPQKYDIPDSVIAFLRGEIAGNPPGGWPEFLRTRALEGRSEKAPLTEVPEEQAH 960

QY 978 DDSKERNSLNRLFLPKPTEEFLEHRRRFGNTSALDDREFFYGLVGEFRLIRLPDVR 1037
Db 961 DDSKERNSLNRLFLPKPTEEFLEHRRRFGNTSALDDREFFYGLVGEFRLIRLPDVR 1020

QY 1038 LLYRLDAISPDGDKMRNVVANNVNGQIRPMVRDRSRVESVYATAEKADSSNKGHVAAP 1097
Db 1021 LLYRLDAISPDGDKMRNVVANNVNGQIRPMVRDRSRVESVYATAEKADSSNKGHVAAP 1080

QY 1098 GYVTVTVAEDEVKAGDAVAIIEMKMEATITASVDGKIERNVVPAAATKVEGGDLI 1157
Db 1081 GYVTVTVAEDEVKAGDAVAIIEMKMEATITASVDGKIERNVVPAAATKVEGGDLI 1140

RESULT 5
US-10-045-072-2
; Sequence 2, Application US/10045072
; Publication No. US20030027305A1
; GENERAL INFORMATION:
; APPLICANT: Sinskey, Anthony J.
; APPLICANT: Lessard, Philip A.
; APPLICANT: Willis, Laura B.
; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
; FILE REFERENCE: 1533.0790002
; CURRENT APPLICATION NUMBER: US/10/045,072
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 09/677,575
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 09/220,081
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-045-072-2

Query Match          98.2%; Score 5759; DB 15; Length 1140;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1133; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 18 VSTHTSSTLPAPKKILVANRGEIATVAFRAALAEATGATVIAIYPREDRGSFHRSEAVR 77
Db 1 MSTHTSSTLPAPKKILVANRGEIATVAFRAALAEATGATVIAIYPREDRGSFHRSEAVR 60

QY 78 IGTEGSPVKAYLDDIIEIGAAKKVADAIYPGYGFLSENAQLARECAENGIITGPTPEV 137
Db 61 IGTEGSPVKAYLDDIIEIGAAKKVADAIYPGYGFLSENAQLARECAENGIITGPTPEV 120

QY 138 LDTGDKSRVTAATAKAGLVLAESTPSKNIDIVKSAEGQTYPIEVKAVAGGGGRMRF 197
Db 121 LDTGDKSRVTAATAKAGLVLAESTPSKNIDIVKSAEGQTYPIEVKAVAGGGGRMRF 180

QY 198 VSSPDELKRLATASREAEAFDGGVYVERAVINPQHIEVQLIGDRTGEVHLVERDCS 257
Db 181 VASPEDELKRLATASREAEAFDGGVYVERAVINPQHIEVQLIGDRTGEVHLVERDCS 240

QY 258 LQRRHQKVVEIAPAQHLDPDLRDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIE 317
Db 241 LQRRHQKVVEIAPAQHLDPDLRDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIE 300

QY 318 PRIQVEHTVTEEVTEVDLVKAQMLAAGATLKGTLTQDKIKTHGAALOCRITTEDP 377
Db 301 PRIQVEHTVTEEVTEVDLVKAQMLAAGATLKGTLTQDKIKTHGAALOCRITTEDP 360

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QY 378 FRPDTCTITAYRSPGAGVRLDGAALGGELTAHFDHSMVLMVKMTCRSDPETAIVARAQAL 437
Db 361 FRPDTGTTITAYRSPGAGVRLDGAALGGELTAHFDHSMVLMVKMTCRSDPETAIVARAQAL 420
QY 438 AETVSGVATNIGFRLALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDIADY 497
Db 421 AETVSGVATNIGFRLALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDIADY 480
QY 498 TVNKPGRPKDVAATIDKLPNTKDLPLPGSRDLKQLGPAFAFADRLREQDALAVDTT 557
Db 481 TVNKPGRPKDVAATIDKLPNTKDLPLPGSRDLKQLGPAFAFADRLREQDALAVDTT 540
QY 558 FRDAHQSLLATRVSRFALPKAAEAVAKLTPELLSSVEAWGGATYDVAMRFLFEDPWRDLDE 617
Db 541 FRDAHQSLLATRVSRFALPKAAEAVAKLTPELLSSVEAWGGATYDVAMRFLFEDPWRDLDE 600
QY 618 LREAMPNVNTOMLLRGNTVGYTTPYDSCVCRFAEVKEAASSGVDFRFDALNDVSMRPA 677
Db 601 LREAMPNVNTOMLLRGNTVGYTTPYDSCVCRFAEVKEAASSGVDFRFDALNDVSMRPA 660
QY 678 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYILKMAEIIYKSAHIIAIDKMAGLLR 737
Db 661 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYILKMAEIIYKSAHIIAIDKMAGLLR 720
QY 738 PAAVTKLVTALREFDLPVHVHTHTAGGOLATYFAAAAGADAVDGCASAPLSGTTSQPS 797
Db 721 PAAVTKLVTALREFDLPVHVHTHTAGGOLATYFAAAAGADAVDGCASAPLSGTTSQPS 780
QY 798 LSAIVAFAHTRDRTGLSLEAVSDLEPYWEAVRGLYLPFESGPGTGRVYRHEIFGGQL 857
Db 781 LSAIVAFAHTRDRTGLSLEAVSDLEPYWEAVRGLYLPFESGPGTGRVYRHEIFGGQL 840
QY 858 SNLRQAATLGLADRELEIDNVAAYNEMIGRTKVTPTSKVYGDALHLVLVAGVDPADF 917
Db 841 SNLRQAATLGLADRELEIDNVAAYNEMIGRTKVTPTSKVYGDALHLVLVAGVDPADF 900
QY 918 AADPQYDIPDSVIAFLRGLGNPPGWPPEPLTRALEGRSEKAPLTVPEVEEQAHLD 977
Db 901 AADPQYDIPDSVIAFLRGLGNPPGWPPEPLTRALEGRSEKAPLTVPEVEEQAHLD 960
QY 978 DSKERNLSNRLFPKPTPEEFLEHRRRFGNTSALDDREFFYGLVGRETLIRLPDVRTP 1037
Db 961 DSKERNLSNRLFPKPTPEEFLEHRRRFGNTSALDDREFFYGLVGRETLIRLPDVRTP 1020
QY 1038 LLVRLDAISEPDDKGMNVVAVNGOIRPMRVDRDSVESVATAEKADSNKGHVAAPFA 1097
Db 1021 LLVRLDAISEPDDKGMNVVAVNGOIRPMRVDRDSVESVATAEKADSNKGHVAAPFA 1080
QY 1098 GVVTVTVAEGDEVKAGDAVAIIEAMKEATITASVDGKIERYVVPVPAATKVEGGDLIVVVS 1157
Db 1081 GVVTVTVAEGDEVKAGDAVAIIEAMKEATITASVDGKIERYVVPVPAATKVEGGDLIVVVS 1140

RESULT 6

US-09-815-242-5468
; Sequence 5468, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Onisen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5468
; LENGTH: 1147
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5468

Query Match 42.4%; Score 2489; DB 9; Length 1147;
Best Local Similarity 45.2%; Pred. No. 3.1e-190;
Matches 527; Conservative 193; Mismatches 383; Indels 62; Gaps 14;

QY 30 KKLIVANRGFIAYRAFAALETGAATVAIYIPREDRSGFSFASAEVRIGTEGSPVKAYL 89
Db 4 KKLIVANRGFIATIRFAAAELDISIVAIYSNEDKSSLHRYKADESYLVGSDGLGPRESYL 63
QY 90 DIDEIIIAKAKKADAIYPGYGFSENAQLARECAENGITFIGTPEVLDTGDKGRAVT 149
Db 64 NIERIIDVAKQANVDATHPGYGFSENEQFARRCAEEGIKFIGPHLEHLDHMFQDKVKART 123
QY 150 AAKAGLPLVLAESTYSKNIDDIIVKSAEGQYPIFYKAVAGCGGRMFRVSSDPELKL 208
Db 124 TALKADLPVPGTDGKIKSYELAKEFAEEAGFPLMKATSGGCGKGMRIYRESELEDAF 183
QY 209 TEASREAAEAGVGSYVVERAVINPOHIEVQILGDRTEGEVHVLYERDCSLQRHQKVEI 268
Db 184 HRAKSAEAKSFGSEVYIERIDNPKHIEVQVIGDEHGNIVHLFERDCSVQRHQKVEV 243
QY 269 APAQHLDELPLRDLICADAVKFCRSIGYGAGTVEFLV--DEKGNHVIEMNPRIQVEHTV 326
Db 244 APSVGLSPTLRQICDAAIOLMENIKYVKNAGTVEFLVSGDE---FFIEVNPVQVEHTI 300
QY 327 TEETVEFDLVKQAMRLAAGATL--KELGLTQDK--IKTHGAALOCRIITWEDPNNGERPDTC 383
Db 301 TEMVTGIDIVKTOILVAAGADLFGEEINMPQOKDITTLGYAIOCRITTEDPLNDFMPDTG 360
QY 384 TITAYRSPGAGVRLD--GAAQLGGEITAHFDSMLVKMTCRSGDFETAVARAQALAEFTV 442
Db 361 TITAYRSGGFGVRLDAGDGFQCAEISPYDYSLLVSLTHAISFKQAEEKWVSRLEMRI 420
QY 443 SGVATNIGFRLALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDIADYVTKNP 502
Db 421 RGVKTNIPFLINVMKNKFTSGDYTKFTETPELEDFIQPSLDRGTKILEYIGNVIN-- 478
QY 503 HGVPRKDVAAPIDKLPIKDLPLP-----RGSRLKQLGPAFAFAD 544
Db 479 -----GFPNVEKRPKPDYELASIPTVSSSKIASFSGTKQLLDEVGPKGVAEW 525
QY 545 LREQDALAVTDTTFRDAHQSLLATRVSRFALPKAAEAVAKLTPELLSSVEAWGGATYDVAM 604
Db 526 VKKQDDVLLTDTTFRDAHQSLLATRVRTKDMINIAASKTADVFKDGFSLFWMWGATFDVAY 585
QY 605 RFLFEDPWRDLDELREAMPNVNTOMLLRGNTVGYTTPYDSCVCRFAEVKEAASSGVDFRI 664
Db 586 NFLKENPWERLERLRKAIPIVLFQMLLRASNAVGYKNYKYPDNVTHKPVQESAKAGIDVRI 645
QY 665 FDALNDVSMRPAIDAVLETNTAVAEVAMAYSGDLSDP--NEKLYTLDYILKMAEIIYK 723
Db 646 FDSLNNVDMQKVAEVAQ--KISEGTCYTGDIILNERSNIYTLLEYIVKLAELEREG 704

QY 724 AHILAIKONAGLURPAATVTKLVIALREFDLPVHVHTDAGQOLATYFAAAQAGADAVD 783
Db 705 PHILAIKDMAGLKPAAVELIGELKAAAYDLPVHLTHDTHDSGNLLTYQAIDAGVDIID 764
QY 784 GASAPLSGTSOPSLSAIYAFAHTTRDTGSLSEAVSDLEPYWEAVRGILYLPFESGTPGP 843
Db 765 TAVASMSGUTSOPANSLSYALNGFPHRLRTDIEGMESLSHYWSTVTRTYSDFESDIKSP 824
QY 844 TGRVYRHEIPGGOLSNLRAQATAGLADRFELTDNYAAVNEMLGRPTKVTSPSSKVVGD 903
Db 825 NTEIYQHEMPGGQYNSLQAKSLGIFGERDEKDMYRVNPLFGDIVKVTSPSSKVVGD 884
QY 904 ALHLVAGVDPADPADPOKIDIPDSVIAPLRGELNPPGGWPEPLRTRALEGRSGKAP 963
Db 885 ALLYMQNDLDEQSVITDYGKLDPFESVWSEFFKIGQPVNGFNKDLQAVILKQGE----A 940
QY 964 LTVPEEEOAHLDDADSKY-----RNSLNRLLPKPTFEFLHRRREGNTSAL 1012
Db 941 LTRPGEYLEPVDVFEKVRLEEEQGPVTEQDIISYLYPKVYEQIOTRQYGNLSLL 1000
QY 1013 DREFFYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMNRNVANVNGQIRPMVRDR 1072
Db 1001 DPTFFFGMNGETVEIEI-DAGKRLIILETISEPDENGRTIYYAMNGQARRIYIKDE 1059
QY 1073 SVESVTATAEKADSSNKGHVAAPFAGVVT-VTVAEGDEVKAGDAVAIIEMKMEATITAS 1131
Db 1060 NVHINANVPKADKSNPSHIGAQMGPSVTEKVSNGETVYKANOPLLITEAMKMETTIQAP 1119
QY 1132 VDGKIERVVVPAATKVEGGDLIVVV 1156
Db 1120 FDGVIKQVTNNGDITATGDLIIIEI 1144

RESULT 7

US-09-815-242-10806
; Sequence 10806, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10806
; LENGTH: 1142
; TYPE: PRF
; ORGANISM: Enterococcus faecalis
US-09-815-242-10806

Query Match 42.0%; Score 2460.5; DB 9; Length 1142;
Best Local Similarity 45.5%; Pred. No. 5.9e-188;
Matches 529; Conservative 187; Mismatches 387; Indels 59; Gaps 17;
QY 30 KKLIVANRGEIIVRAFAALETGAATVAYIPREDRGSFHRSEAFSEAVRIGTEGSPVKAYL 89
Db 2 KKLIVANRGEIIVRAFAALETGAATVAYIPREDRGSFHRSEAFSEAVRIGTEGSPVKAYL 89
QY 90 DIDEIIGAAYKADAIYPCYGFSLSENAQALARECAENGITFTGPTPEVLDTLGDCKRAV 149
Db 62 DIENIIQIAKKSGADAIHPYGFSLSENAQALARECAENGITFTGPTPEVLDTLGDCKRAV 149
QY 150 AAKKAGLPLVLAEST-PSKNIDIDIVKSAEGTQPIFYKAVAGGGGGRGWRVSSDELRKLA 208
Db 122 AAVAAGIASIPGSDGPVATVEVAFGETHGPIMIKAAALGGGGRGWRVVAHDAKEAREGY 181
QY 209 TEASREAAAFGDSGVYVERAVINPOHIEVQILGDRTEGVVHLYERDCSLQRHQKVEI 268
Db 182 ERAKSEAKAAGSDEYVEYKISNPKHIEVQILGDHGNVHLFERDCSVQRHQRKVEV 241
QY 269 APAQHLDPRLDRICADAVKFCRSIGYOGAGTVERFLVDEKGNHVFTEMNPRIQVEHTVE 328
Db 242 APCVSNNEORAAICSAAYQLMAHVGVNAGVEFLV-EGDQFYFIEVNPVQVEHTITE 300
QY 329 EYTEVDLVKAQMLAAGATL-KELGL-TQDKIKTHGAALQCRITTEDPNNGRFPDGTIT 386
Db 301 MITDIDIVISQIAQGLDLHKMHLPKQNLTKGAAIQCRITTEDPNNGRFPDGTIT 360
QY 387 AYRSPGAGVRUD-GAAQLGGEITAHFDSMLVKMTCRSGDSDFETAVARAQALAEFTVSGY 445
Db 361 TYRSPGAGVRUDVGNAYSGYAVTPYFDSLLVKVCTHGFSGFQAISKMRCKLEFRIRG 420
QY 446 ATNIGFLRALLREEDFTSKRIATGFTGDHPHLLQAPPADDEQGRIDLDYLVTVNKPVG 505
Db 421 KTNIPFLQNVVSPAFQSGEAKTTFIDNTPELFEPRMRDRGNKTKMYIGEVTNPGFI 480
QY 506 R-----PKDVAAPIDKLPNIKOLPLPRGSRDLKQLGPAFAFARDLREQDALV 553
Db 481 ERTEKKYFEAPRVPTDIEVP-EKVIITAKNI-----LDAQGATAVIDWVKNOESVLM 530
QY 554 TDTFRDAHQSLAVRVRSFALKPAEAAVAKLT-----PELLSVEAWGGATYDAMRFLPE 609
Db 531 TDTFRDAHQSLAVRVRTQDFK---AAGLTDVALPELFSEMMGGATFVAVRFLTE 586
QY 610 DPWRDLDELREAMPNVNIQMLLRNTVGYTPYPSVCRAFYKEAASSGVDFIRFDALN 669
Db 587 DPWRDLDELREAMPNVNIQMLLRNTVGYTPYPSVCRAFYKEAASSGVDFIRFDALN 646
QY 670 DYSOMRPAIDAVLENTAVAEVAMAYSGDSDPNKLYTLDYLLKMAEIVSGAHILAI 729
Db 647 WIPOMEKSIQVVRDTG-KIAEAAICYTGIDINPARAKYVNOYIYLDMAKELENLGAQIIAI 705
QY 730 KDMAGILLRPAAVTKLVTLRRREFDLPVHVHTDAGQOLATYFAAAQAGADAVDASAPL 789
Db 706 KDMAGILLRPAAVTKLVTLRRREFDLPVHVHTDAGQOLATYFAAAQAGADAVDASAPL 765
QY 790 SGTTSQPSLSAIVAAFAHTRDTGLSLEAVSOLEPYWEAVRGILYLPFESGTPGTRVYR 849
Db 766 SGTTSQPSLSAIVAAFAHTRDTGLSLEAVSOLEPYWEAVRGILYLPFESGTPGTRVYR 825
QY 850 HEIPGOLSNLRAQATAGLADRFELTDNYAAVNEMLGRPTKVTSPSSKVVGDALHLVG 909
Db 826 HEMPGQYNSLQAKSLGIFGERDEKDMYRVNPLFGDIVKVTSPSSKVVGDALHLVG 885
QY 910 AGVDPADFAADPKYDIPDSVIAFLRGELNPPGGWPEPLRTRALEGRSGKAPLTVPE 969
Db 886 NHTEQDYVARGEEELSFESVVTFFQDGLQGVGFGPKELQRIILKGR----PATERPG 941
QY 970 EQAHLDDADDSKER-----RNSLNRLLPKPTFEFLHRRREGNTSALDDR 1015
Db 942 DLAAFPVDFAKVQOEELAEKIGYQPKLEEVLSYLMYP---QVFEYRQKYVETFGDITLDT 998
QY 1016 EFFYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMNRNVANVNGQIRPMVRDRSVE 1075

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Db 999 TEFNGROGETLEVOIERGKT-LIIRLDEIGEPIIDGNRVLFNNGRREVVLVKDASIK 1057
QY 1076 SVTATAEKADSSNKGHVAPFAG-VVTVVVAEGDEVKAGDAVAIIIEAMKWEATITASVDG 1134
Db 1058 SAVQVQKAEPIKNGEIGATMSGVLOVLVYKRGDKVEKGQPLLIIEAMKMETTIEARFAG 1117
QY 1135 KIIEVVVPAATKVEGGDLIVVV 1156
Db 1118 TVDHIYVEGEAISGDLLEVV 1139

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RESULT 8

```

US-09-815-242-12361
; Sequence 12361, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlisen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12361
; LENGTH: 1073
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12361

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Query Match 39.2%; Score 2300; DB 9; Length 1073;
Best Local Similarity 44.8%; Pred. No. 4e-175;
Matches 489; Conservative 180; Mismatches 360; Indels 62; Gaps 14;

QY 104 DAHPYGYFLSNAOLARECAENGITFPGTPEVLDTGDKSRVTAACKAGLPVL-ABS 162
Db 2 DAHPYGYFLSNEQFARRCAEEGKIFGPHLEHDMFGDKVKARTAIKADLPVPGTD 61
QY 163 TSPKNIDDIKSAEGQTPYFVAVAGGGGGRGMRVSSPDDELKRLATEASRAEAFGDG 222
Db 62 GPIKSYELAKEFAEAGFPLMTKATSGGGGKGMRIVRESELEDAFHRAKSAEKSFGNS 121
QY 223 SVYVERAVINPOHIEVOILGDRGTGEVHLYERDCSLQRHQKQVETAPAHLDPELRDRI 282
Db 122 EYVIERIDNPHIEVQVIGDEHGNIVHLFERDCSVQRHQKVEVAPSGVLSPLIQRRI 181
QY 283 CDAAVKFCRSIGYQAGVEFLV--DEKGNHVFIEHNPRIQVEHVTVEVVDLVKAQM 340
Db 182 CDAAIQLMENIKYVNAVTEFLVSGDE---FFFIEVNPVQVEHITTEMTVDIVKIQI 238
QY 341 RLAAAGATL--KELGLTQDK-IXTHGAALOCRTTTPDNNNGFRPDGTITAYKSPGAGVR 397

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Db 239 LVAAGADLGEFEINMPQOKDITTLGLVAIQCRITTEDPLNDFMPDGTIIAYRSSGGFVR 298
QY 398 LO-GAAGLGEIITAHFDSMLVKMTCRSGDPFETAVARAQALAEFTYSGVATNTIGFRLAL 456
Db 299 LDAGDGOFAQAEISPYSDSLVKLSTHAISFKQAEKMRVSRLEMRINGVKTNPFLNVM 358
QY 457 REEDFTSKRIATGFIGDHPHLLQAPDADDEQGRILDYADVTYVKNKPHGVKPKDVAAPIDK 516
Db 359 KNAKFTSGDYTTKFIETPELFDIQPSLDRGTTLLEYIGNVTIN-----G 403
QY 517 LPNIKDLPLP-----RGSRLKQLGPAAPAFARDLEQDALAVTDTTF 558
Db 404 FPNVEKRKPDYELASIPTVSSSKIASFSCTQLLDEVGPKGVAEWWKQDDVLLTDTTF 463
QY 559 RDAHQSLLATRVRSFALKPAEAAVAKLTPELLSVERAWGGATYDVAMRFLFEDPDWRLDEL 618
Db 464 RDAHQSLLATRVRTKDMINIAKTADVFKDGFLEMMWGGATFOVAYNFLKENPWERLERL 523
QY 619 REAMPNVNIQMLLRGNTVGYTPYDPSVCRAFYKEAASSGVDTFRIFDALNDYSQMRPAI 678
Db 524 RKAIPNVLFQMLLRASNNAVGYKNYDNVHKFVQESAKAGIDVFRIFDSLNWVDQMKVAN 583
QY 679 DAVLENTAVAEVAMAYSGDLSDP-NEKLYTLDYLYLKMAEEIVKSGAHILAIKDMAGLLR 737
Db 584 EAVQEAG-KISEGTICYTGDLNPNERSNIYTYLVYVYKLAKELEREGFHILAIKDMAGLLK 642
QY 738 PAAVTKLVTLALRREFDLPHVHTHTAGGOLATYFAAAGADAVGASAPLSGTTSQPS 797
Db 643 PKAAVELIGELKAAVDLPILHHTHTDSGNLLTYKQADAGVDIIDTAVASMSGLTSQPS 702
QY 798 LSAIVAAFAHTRRDTGLSLEAVSDLEPYEAVRGLYLPFESGTPPGTGRVYRHEIPGGOL 857
Db 703 ANSLYALNGFPHLPTDIEGMESLSHYSTVYTYSDPESDIKSPNTELYQHEMFGGQY 762
QY 858 SNLRAQATALGLADREFELIEDNYAENVMLGRFTKTPSSKVYVGDIALHLVAGVDPADF 917
Db 763 SNLSQAQKSLGLGERPDEKVMYRRVNFGLDVKVTPSSKVYVGDIALYVQNDLDEQSV 822
QY 918 AADPKYDIPDSVIAFLRGELGNPPGWPPEPLTRALEGRSEKAPLTEVPEEQAHIDA 977
Db 823 ITDGYKLDPPESVVSFFKGIQPVNGFNKDLQAVILKGQ-----ALTARPGYLEPVDV 878
QY 978 DDSKE-----RRNSLRLLFPKTEEFLEHRRFRFGNTSALDDREFFYGLVEGRE 1026
Db 879 EKVRELLEEEQOQPVTEQDIISYVLYPKVYEQIQRNOYGNLSLDTTFTFFGMNGET 938
QY 1027 TLIRLPDVRTPILLRLDAISEPDDKGMNRNVANVNGQIRPMRVDRSRSVSTATAEKADS 1086
Db 939 VETEI-DKGKRLIILETISEPDENGNTIYVAMNGQARRIVIKDENVHTNANVKPKADK 997
QY 1087 SNKGHVAAPFAGVVT-VTVAEKDEVKAGDAVAIIIEAMKWEATITASVDGKIERYVVPAT 1145
Db 998 SNFSGHGAOMPQSVTEKVSQVGTETKANQPLLIIEAMKMETTIIQAPFDGVIVKQVNNGD 1057
QY 1146 KVEGGDLIVVV 1156
Db 1058 TIATGDLLEI 1068

```

RESULT 9

```

US-09-767-479-6
; Sequence 6, Application US/09767479
; Patent No. US20010036654A1
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
; METHODS OF USE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433

```


QY 268 IAPAOHLDPRLDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFTEMNPRIQVHEHTV 327
 Db 242 EAPSPALSDLRKQMGDAVKVAQAIGYIGAGTVEFLVDATGNTFYEMENMTRLOVEHPVT 301
 QY 328 EEVTEVDLVKAQMRILAAGATLKLGLTQDKIKTHGAALOCRTTTPDNNPFRPDGTGTTA 387
 Db 302 EMITGLDLAEQIRIAQGEALR---FROADIQLRHAIECRINAEDPEYFNFRPNPGRITG 358
 QY 388 YRSPGGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTVSGVAT 447
 Db 359 YLPPGGPGVVDVSHVYTDYEIPYDLSLGLKLVWGATREEARQALRECAITGLPT 418
 QY 448 NTGFLRALLREEDFTSKRIATGFI 471
 Db 419 TILSPHQLMOMPEFLRGELYTNFV 442

RESULT 11

US-09-815-242-5215
 ; Sequence 5215, Application US/09815242
 ; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011a

; CURRENT APPLICATION NUMBER: US/09/815,242
 ; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-05-23

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-10-23

; PRIOR FILING DATE: 2000-11-27

; PRIOR FILING DATE: 2000-12-22

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5215

; LENGTH: 471

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-815-242-5215

Query Match 16.7%; Score 979.5; DB 9; Length 471;

Best Local Similarity 45.9%; Pred. No. 7.9e-70;

Matches 209; Conservative 74; Mismatches 157; Indels 15; Gaps 6;

QY 30 KKLIVANGETIAVAFRAALETGAATVAIYPREDRGSFHRFSFASAVRIGTEGSPVKAYL 89

Db 3 KKLIVANGETIAVAFRAALETGAATVAIYPREDRGSFHRFSFASAVRIGTEGSPVKAYL 89

QY 90 DIDEITGAKKVKAADAIYPGYGFLSENAQALARECAENIGITGTPPEVLDTLIGDKSRVAT 149

Db 61 NPLRVNLAVSGCDALHVGFGYFLSENAELAEICAEIRGKIFGSAQVIRRMGDKTEARR 120

QY 150 AAKKAGLPVLAESTPSK---NIDDI---VKSAGQGYPIFVKAAGGGGGRGMRFYSSPDEL 204

Db 121 SMIAAGVP---CTPGTSGNVADLAELAREARICGYFWLKRATSGGGGGRGIRRCNSREEL 176

QY 205 RKLATEASREAEAFAGDGVYVERAVINPQHIEVQILGDRTEGVVHLYBEDCSLOREHOK 264
 Db 177 EQAPPRVISEAKAFGSAEVELEKCIIVNPKHIEAQILADSFQNTVHLFERDCSIQRNQK 236
 QY 265 VVEIAPAOHLDPRLDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFTEMNPRIQVHEH 324
 Db 237 LIEIAPSPQLTPEQRAYIGDLAVRAAKAVGENAGIVEFLLAD-GEVYFEMENMTRLOVEH 295
 QY 325 TVTEEVTEVDLVKAQMRILAAGATLKLGLTQDKIKTHGAALOCRTTTPDNNPFRPDGTG 384
 Db 296 TITEETITGDIVVREQIRIASGL---ELSVKQDDIVHRGYALOFRIANAEDPPKNFLFSPFG 352
 QY 385 ITAYRSPGGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTVSG 444
 Db 353 ITRYAPGGPGVVDVSHVYTDYEIPYDLSLGLKLVWGATREEARQALRECAITGLPT 418
 QY 445 VATNIGFLRALLREEDFTSKRIATGFI 479
 Db 413 VKTTPYYQELRNPEFRSGQFNTSFVESHPELTQ 447

RESULT 12

US-09-815-242-13885
 ; Sequence 13885, Application US/09815242
 ; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011a

; CURRENT APPLICATION NUMBER: US/09/815,242
 ; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-05-23

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-10-23

; PRIOR FILING DATE: 2000-11-27

; PRIOR FILING DATE: 2000-12-22

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13885

; LENGTH: 449

; TYPE: PRT

; ORGANISM: Salmonella typhi

US-09-815-242-13885

Query Match 16.3%; Score 956; DB 9; Length 449;

Best Local Similarity 47.6%; Pred. No. 5.6e-68;

Matches 206; Conservative 61; Mismatches 158; Indels 8; Gaps 5;

QY 31 KILVANGETIAVAFRAALETGAATVAIYPREDRGSFHRFSFASAVRIGTEGSPVKAYL 90

Db 4 KIVIANRGEIALRILRACKELGKIVAVHSSADROLKHLVLLADEVFCIGPAPS-VKSYLN 62

QY 91 IDEITGAKKVKAADAIYPGYGFLSENAQALARECAENIGITGTPPEVLDTLIGDKSRVAT 150

Db 63 IPAISAAEITGAVAIHPGYGFLSENAFNAFQVRSFGIFIGPKADTIRLMGDKVSAITA 122

Db 181 WERVRRVTAASFSSAGIFLERLHARHVEVQVGDGRVVTLLGDRDCSLQRNOKVVE 240
QY
Db 268 IAPAHLDPRLDRICADAVKFCISGYCAGIVEELVD-EKGNHVFIEHNPRIQVHTV 326
QY
Db 241 EAPAGLPSVHRDLASANDLCAAGYRSAGIVFVYDAAREEAYELEVNTRLQVHPV 300
QY
Db 327 TEEVTEVDLVKAQMLAAGATLKLGLTODKIKTHGAALQCRITTEPNNGFRPDTGIT 386
Db 301 TEEYGVDLVAMLRAGG---DAVVVRDPGRGHAVEARYAEDPSREHPSAGLLT 356
QY
Db 387 AYSPGGVRLDGAOLGGEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTVSGVA 446
Db 357 RVBEP--QGVYRVDGWETGTVEVTSYDPMKAVVYSGDRAHALARLEALATRDVGDIE 414
QY
Db 447 TNIGFLRAL---LREEDFTSKRIA-----TGF--IGD 473
Db 415 TNLGLVRAALADHGLRTATHTTALAKITDPTPRVEVVAAGTITTVODMPCRTGYWQGV 474
QY
Db 474 HPHLLQAPPADD-----EQR-----ILDYLDVTVN 500
Db 475 PP---CGPMDDRSFRIGNALNEEGAPGLECTLRGPALRFTHATVTCVYGAPVTV 530
QY
Db 501 KPHGVKPDVAAIDKL-----PNIKDPLPRGSRDLKLGPAAF-----A 542
Db 531 GTPVAQWEPVTVPAGALLEVCAPAEPCLRVYVLFAGGLDVPAPFLGSAATFTLGRFGHGG 590
QY
Db 543 RDLREQDALAVTDTTFRDA-----HOSLLATRVRSFALKPAAEAVAKLIPELLSVWAGG 597
Db 591 RALRTGDVLHGSSVTDGAPVPAGDRPVFAETHVGALEGPAAPEFTED---DIRDYA 648
QY
Db 598 AYDV-----AMRFLFEDP-WDRLEDELREAMPNVIQMLLRNTVGYT---PY--P 643
Db 649 AGKVFHFSARTGVRLVGPKPWARSDDGEGALHPSNIHDTTPYSVGAVDYGDMPVLLGP 708
QY
Db 644 DS-----VCRAFVKEAASGVDFIRFALNDVDSMRPAIDAVLNTNVAEAVMAYSG 697
Db 709 DGBSLGGFCVCPATVATAEKW-----KLQLRPG-DTVRET----- 742
QY
Db 698 DLSDDPNEKLYTLDYLYLMAEIVKSGAHILAIDMAGLLRPAVT-----KLYALR 749
Db 743 -----PLAEDGSTPAIVDGGVLARDGDTVYRRSGDDMLLVFEPG 782
QY
Db 750 REDFLPVHHTHTAGGQATYFAAAQAGADAV-----DGASAPLSGTTSQ 795
Db 783 MOLDLALRMVH-----ALMEAAEAGLDGVTDLTPGIRSLQIRTPRLPLR----- 830
QY
Db 796 PSLSAIVAAFAHTRDTGLSLAVSLPEYWEAV---RGLYLPFESGTPGPTGRVYRHEI 852
Db 831 -ELLAVR-----ETVSALPTDQLVPSRTVHLPLSLWDDPATREAIERY-- 874
QY
Db 853 PGGQLSNLRQA-----TALGLADRFELIEDNYAAVNE---MLGRPTKVTIPSSKVYV 901
Db 875 ---MAGVRDDAPWCPWNIEFIRRVNGLESVADVDTVDFAEYLVLG-----LG 919
QY
Db 902 DLALHLVAGVDPADPAADPQ-----KYDIPDSVIAFLRGELNP-----PGWP 946
Db 920 DWYL---GA---FVATPLDPRHLVTTKYNPARTWAENSUGVIGAYLCVYGMGPGGYQ 973
QY
Db 947 EPLRTRALBGRSEKAPLTPVPEEQAHLDADDSEKRRNSLKLFPKPTFELEHRRRF 1006
Db 974 FVGR-----TQVWSGQ-----QGF-----EPGSPWL---LRF 1001
QY
Db 1007 GNTSALDDREFFYGLVGRETLRL--PDVVRTPLLVRLDAISPPDDKGMNVVANVNGQIR 1065
Db 1002 -----FDRIKWAV--GPELDDLRLADIASGRFVPRVEGEFSIAGYESFLAANAGSTA 1053
QY
Db 1066 PMVR-----DRSVESVTATAEKADSSNKGHVAAPFAGVVT-----VT 1103
Db 1054 AFRAGQAAFAAERDAWEAAGEFARAEEAATAEAPPAEVTVPVGGALVEAFEAASWQLN 1113
QY
Db 1104 VAEGDEVKAGDAVAILIEMKMEATITASVDGKIERYVVPVPAATKVGGLIVVVS 1157
QY

Db 1114 VGPDAVYTAGPILLTLEAMKMSRVPAAGVYVTEILARPQDQVAGTALVWLA 1167
RESULT 15
US-09-815-242-10330
; Sequence 10330, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10330
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-815-242-10330
Query Match 16.0%; Score 940; DB 9; Length 449;
Best Local Similarity 46.8%; Pred. No. 1,1e-66;
Matches 203; Conservative 66; Mismatches 155; Indels 10; Gaps 6;
QY 31 KILVANGETIYAVRAFAALETGAATVAIYPRDRGFSFHSFASAEVRICTEGSPVKAYLD 90
Db 4 KIVIANRGEIALRILRACKELGIKTVAVHSSADRLKHLLADETVCIGPAPS-VKSYLN 62
QY 91 IDEITGAKKVADAIYPGYFELSENAQLARECAENGITFPTPEVLDLTGDKSRAVTA 150
Db 63 IFATISAAAITGAVAIHPGYFELSENAFNAFQVRSFIFIGPKARTILMGDKVSALAA 122
QY 151 AKKAGLPVLAESTPSKNIDIVKS---AEGQYPIPVKAVAGGGGGMFVSSPDRLKL 207
Db 123 MKKAGVPCVPSDGLPG--DDMKNRALAKRIGYPIIKASGGGGGGMKVRVGDDELAOS 181
QY 208 ATEASREAAFAFGDSVYVERAVINPQHIEVQILGDRTEGVVHLXERDCSLORRHQKVE 267
Db 182 ISWTRAEAAKAFASNDVMYMEKYLENPRHVEIQVLADGGQNAIYLAERDCSMQRHOKVVE 241
QY 268 IAPAHLDPELDRICADAVKFCISGYCAGIVEELVD-EKGNHVFIEHNPRIQVHTV 327
Db 242 EAPAGITPELRYRIGERCAKACVDIGYRGAGTFFELF-ENGFEYFIEMNTRIQVHPVT 300
QY 328 ESWTEVDLVKAQMLAAGATLKLGLTODKIKTHGAALQCRITTEPNNGFRPDTGITTA 387
Db 301 EMITGVDLIKELRLAAG---QPLSIKQEVHVRHAVECRINAEDPNT-FLPSPGKITR 356
QY 388 YRSPGGAGVRLDGAALQGEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTVSGVAT 447

Db 357 FHAPGGGVWESHYAGYVPPYDSDMIGKLCYGENRDVAIARMKNALQELIIDGIKT 416
QY 448 NIGFLRALLREDF 461
|: :|:|
Db 417 NVDLQIRIMDNDF 430

Search completed: September 24, 2003, 15:53:07
Job time : 44.7701 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3713.5	63.3	1127	2	D70671	pyruvate carboxyla
2	2550.5	43.5	1178	1	A4755	pyruvate carboxyla
3	2548.5	43.5	1178	2	JC4351	pyruvate carboxyla
4	2535.5	43.1	1150	2	A83978	pyruvate carboxyla
5	2530	43.2	1148	2	F69695	pyruvate carboxyla
6	2528.5	43.1	1178	1	JC2460	pyruvate carboxyla
7	2494	42.5	1146	2	AH1208	pyruvate carboxyla
8	2491	42.5	1146	2	AC1565	pyruvate carboxyla
9	2490.5	42.5	1145	2	D97227	pyruvate carboxyla
10	2489	42.4	1150	2	G89881	pyruvate carboxyla
11	2474.5	42.2	1174	2	AE2911	pyruvate carboxyla
12	2474.5	42.2	1174	2	C97686	pyruvate carboxyla
13	2465.5	42.0	1158	2	AE3285	pyruvate carboxyla
14	2461	42.0	1175	2	T20346	pyruvate carboxyla
15	2457	41.9	1178	1	QXBYP	pyruvate carboxyla
16	2447	41.7	1185	2	T39734	pyruvate carboxyla
17	2436	41.5	1180	2	S46094	pyruvate carboxyla
18	2417.5	41.2	1195	2	T43735	pyruvate carboxyla
19	2413	41.1	1137	2	E86708	pyruvate carboxyla
20	2119.5	36.1	984	2	T44608	pyruvate carboxyla
21	1079	18.4	501	2	D64453	biotin carboxylase
22	1071.5	18.3	477	2	G70427	biotin carboxylase
23	1040	17.7	472	2	A70432	biotin carboxylase
24	1032.5	17.6	447	2	A53311	biotin carboxylase
25	1032.5	17.6	447	2	AH1923	biotin carboxylase
26	1020	17.4	506	2	D69277	biotin carboxylase
27	996	17.0	491	2	A69223	biotin carboxylase
28	979.5	16.7	471	2	G82966	probable biotin ca
29	978.5	16.7	448	2	S74380	biota carboxylase

QY 209 TEASREAEAFGSGSVYVERAVINPOHIEVQILGDRTEGVVHLHYERDCSLQRRHQKVEI 268
 Db 182 EASREAEAFGSGSVYLEQAVINPRHIEVQILADNLGDIHLYERDCSVQRHQKVEI 241
 QY 269 APAQHIDPELRDRICADAVKFCRSIGVGAGTVEELVDEKGNHVFTEMNPRIOVEHVTE 328
 Db 242 APAPHLDAELRYKMCVDNAFAHIGYSCTAGTVEFLDERGEVVFTEMNPRIOVEHVTE 301
 QY 329 EVTEVDLVKAQMLAAGATLKEGLTQDKTKTHGAALQCRITTEDPNNRFRPDTGITAY 388
 Db 302 EITDVLVLSQRLAAGEITELQGLRQEDTAPHGAALQCRITTEDPANGFRPDTGRISAL 361
 QY 389 RSGGAGVRLDGAQGLGETTAHFDMLVKMTCRGSDFETAVARAQALAEFTVSGVATN 448
 Db 362 RTAGGAGVRLDGTNLGAETSPFDMSMLVKLTGRDLPTAVSRARRATAEFTVSGVSTN 421
 QY 449 IGLRALLREEDFTSKRIATGFIQDHPHLLQAPADDEQGRILDYLDVTVNKGPHVRPK 508
 Db 422 IFLQAVLDPDFRAGRVITSFIDERPQLLTARASADRGTKIINFADVTVNNPYSRPS 481
 QY 509 DVAAPIDKLNKIDPL-----PRGSRDLKQLGPAAPARDLREQDALAVTDTTFRDAHQ 564
 Db 482 TI-YPDKLP--DLDLRAAPPAGSKORLVKLGPEGFARWLRESAAVGVTDTTFRDAHQ 537
 QY 565 LLATRVRSFALKEAAEAVAKLTPELLSVEANGCATYDVAMRFLFEDPDRLDELREAMPN 624
 Db 538 LLATRVTSLSRVAPYLARTMPPOLLSVCEWGGATYDVALRFLKEDPWERLATLRAAMPN 597
 QY 625 VNQMLLRGNTVGYTYPDVSVCRAFVKEAASGVDFIRFDALNDVDSQMRPAIDAVLET 684
 Db 598 ICLQMLLRGNTVGYTYPPEIVTSFVQETATGIDIFRFDALNIESMRPAIDAVRET 657
 QY 685 NTAAVEAVMAYSDLSDPNEKLYTLXYLKMAEETVKSAGHIIAIDKMGALLRPAAVTKL 744
 Db 658 GSAIAEVAMCYTGDLDPCEQLYTLXYLKABQIVDAGAHVIAIDKMGALLRPPAAQRL 717
 QY 745 VTALRREFDLPVHVHTDAGGOLATYFAAAQAGADAVDGCASPLSTTSQPSLSALVAA 804
 Db 718 VSALRSRFDLPVHLHTDTPGGQLASYVAWHAGADAVDGAAPLAGTISQPALSSIVAA 777
 QY 805 FAHTRDGTGLSEAVSDLEPYWBAVRGLXLPFESGTPGTRVYRHEIFGGQLSNLRQA 864
 Db 778 AATHEXDTGLSVAVALPEYWEALRKYVAPFESGLPGTRVYHHEIFGGQLSNLRQA 837
 QY 865 TALGLADRELIEDNTAAVNMELGRPTKVTSPSKVVDGLALHLVGAVDPADFAADPKY 924
 Db 838 IALGLDGRFEETBEAYAGADRVLGRVVKVTPSTSKVVDGLALALVGAVSADFAADPARF 897
 QY 925 DIPDSVIAFLRGLNPPGGWPEPLRTRALEGRSEKAPLTVPEEEOAHLDAADDSKERR 984
 Db 898 GIPESVGLRGLGELGPPGGWPEPLTAALAGGAAR-PTAQLAODETALSVGAK-RQ 955
 QY 985 NSLNRLLFPKPEETFEHRRRGNTSALDDREFFYGLVGEFRETILRDPVTRPLLVRLDA 1044
 Db 956 ATNLRLLFPSPKEEHEAREYAGDTSQLSANQFPYGLRQGEHRVKL-ERGVELLIGLEA 1014
 QY 1045 ISEPDGKMRNVYVANGQIRMRVDRSVESVTATAEKADSNKCHVAAPAGVTVTV 1104
 Db 1015 ISEPDGKMRVCMILNGQLRVLVDRSTASAVPAEAKADRNPGHIAAPAGVTVTV 1074
 QY 1105 AEGDEYKGDVAVAIIEAMKEATITASVDGKIERYVVVPAATKVEGGDLIVVVS 1157
 Db 1075 CVGERVAGOTIATIEAMKEAPITAPVAGTVERVAVSDTAQVEGGDLIVVVS 1127

RESULT 2

A47255

pyruvate carboxylase (EC 6.4.1.1) precursor [similarity] - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Feb-2002

C:Accession: A47255

R:Zhang, J.; Xia, W.L.; Brew, K.; Ahmad, F.

Proc. Natl. Acad. Sci. U.S.A. 90, 1766-1770, 1993

A;Title: Adipose pyruvate carboxylase: amino acid sequence and domain structure deduc
 A;Reference number: A47255; MUID:93189578; PMID:8446588
 A;Accession: A47255
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1178 <ZHA>
 A;Cross-references: GB:109192; NID:g293743; PIDN:AAA39737.1; PID:g293744
 A;Experimental source: 3T3-L1 adipocytes
 C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bindi
 C;Keywords: biotin binding; ligase; mitochondrion
 F;1-20/Domain: transit peptide (mitochondrion) #status predicted <TRP>
 F;21-1178/Product: pyruvate carboxylase #status predicted <MAT>
 F;39-494/Domain: biotin carboxylase homology <BCH>
 F;1105-1178/Domain: lipoyl/biotin-binding homology <LPB>
 F;1144/Binding site: biotin (lys) (covalent) #status predicted

Query Match 43.5%; Score 2550.5; DB 1; Length 1178;

Best Local Similarity 46.1%; Pred. No. 2.6e-132;

Matches 543; Conservative 192; Mismatches 407; Indels 35; Gaps 13;

QY 7 GGLLLKGITLVSTHTSSSTLPA-----FKKILVANRGEIAVRAAFRAALGTGA 54
 Db 9 GGLRLLGV-----RSSSNAPVAPNVRLEYPIKKVMVANRGEIAIRVFRACTELGR 62
 QY 55 TVAIYPLEDRGSRHRSFASAVRIGTEGSPVKAYLDITDELIGAAKKVKADAIYPGYGLS 114
 Db 63 TVAVYSEQDTGQMRHQKADAEAYLIGRGLAPVQAYLHLPDIILKVKAKENGVDVHPGYGLS 122
 QY 115 ENAQLARECAENIGITGTPTEVPELDITGDKSRAYTAAGKAGLPVL-AESTPSKNIDDIIVK 173
 Db 123 ERADFAQACODAGVRFIGPSPVVRKMGDKVEARAIAAGVVPVPTGSPISLSHEAHE 182
 QY 174 SARGQYPIFVKAVAGGGGRMRFVSPDELRLATEASREAAAFGDSGVYVERAVINP 233
 Db 183 FSNTEGFPIIFKAYGGGGRMVRVSHYELEENYTRAYSEALAAFGNGALFVEKTEKP 242
 QY 234 QHTEVOILGDRTEGVVHLRYERDCSLORRHKVVEIAPAOHLDPDELDRICADAVKPCRSI 293
 Db 243 RHEVOILGDOYGNILHLRYERDCSLORRHKVVEIAPATHLPDLQSLRSLTSDSVKIAQV 302
 QY 294 GYGAGTVFELVDEKGNHVFIEENPRIOVEHTVTEVTEVDLVKAQMLAAGATLKEGL 353
 Db 303 GYENAGTVFELVDEKGNHVFIEENPRIOVEHTVTEVTEVDLVKAQMLAAGATLKEGL 362
 QY 354 TQDKITHGAALQCRITTEDPNNRFRPDTGITIAYRSPGAGVRLDGAAL-GGEITAHF 412
 Db 363 RQENIRINGCAIQCRVTTEDPARSFQDPTGRIEVRSGEGMGIRLDNASAFQAVISPHY 422
 QY 413 DMLVKMTCRGSDFETAVARAQALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFTG 472
 Db 423 DILLVVKVIAHGKDHPHTAATKMSRALAEFRVGVKTNIPFLQVNNQOQLAGTVDTFD 482
 QY 473 DHPHLLQAPADDEQGRILDYLDVTVNKGPHVRPKDVA-APID-KLPNIKDLPGRGR 530
 Db 483 ENPELFQLRPAQNRAQKLLHLYGHVMVNGTPTPIPVNVSFSPVDPAVPVPGPPAGFR 542
 QY 531 DLKQLGPAARADLRQEDALAVTDTTFRDAHQSLIATRVRSFALKPAEAEVAKLTPELL 590
 Db 543 DILLREGPGGFARVNRHOGILLMDTTFRDAHQSLIATRVTRTHDKLKIAPYVAHNENKLF 602
 QY 591 SVEANGGATYDVAMRFLFEDPDRLDELREAMPNVMOMLLRGRNTVGTPTPYDSVCRAF 650
 Db 603 SMENMGATYDVAMRFLFECPPRRRLQELRELIPNPFQMLLKGANAVGNTIPDNVVPKF 662
 QY 651 VKEAASGVDFIRFDALNDVDSQMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLD 710
 Db 663 CEVAKENGMDVFRVFDLSNLYLNNMLLGMEEAGSAG-GVVEAALSYTGDVADPSRTKYSLE 721
 QY 711 YILKMAEETVKSAGHIIAIDKMGALLRPAAVTKLVLTALRREF-DLPVHVHTHDTAGQOLA 769
 Db 722 YYMGLAEELVRAGTHILCIKDMAGLLKPAACCTMLVSSLRDRPDLPLHITHDTSGAGVA 781

Db 962 PFRSKVLKDLPRIEGRPGASLPPLNLKLEKDLIDRHGEVTPEDVLSAAMYPDVFAQFK 1021
 QY 1001 EHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVRPLIVRLDAISEPDDKGRNVVAVY 1060
 Db 1022 DFATGGLDLSLRLFLQGPKTABEFVELEKGT-LHKALAVSOLNRRAGORQVFFEL 1080
 QY 1061 NGQIRPMVRDRSVESVTAFAEKADSSNGKHVAAPFAG-VVTVTVAEGDEKAGDAVAII 1119
 Db 1081 NGQLRSLIVKDTQAMKEMHPKALKADVKQIGAPMPGKVIDVKVAAGAKVVGKQPLCVL 1140
 QY 1120 EAMKEATITASVDGKIERVVVVAATKVEGGDLIVVV 1156
 Db 1141 SAMKETVVTSPMEGTIRKVVHTKMTLEGDDLILEI 1177

RESULT 4
 A83978
 pyruvate carboxylase pycA [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: A83978
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1150 <STO>
 A:Cross-references: GB:AP001516; GB:BA000004; MID:g10175192; PIDN:BA06344.1; GSPDB:GN00
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: pycA
 C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 43.2%; Score 2535.5; DB 2; Length 1150;
 Best Local Similarity 46.9%; Pred. No. 1.7e-131;
 Matches 540; Conservative 185; Mismatches 399; Indels 27; Gaps 13;

QY 26 LPFAKKILVANRGEIAVRAFALETAATVAIYREDGRSGFHRSPASAVRIGTEGSPV 85
 Db 4 LKNKKVLVANRGEIAIRFRACTELHIRTVAIYSKEDTGAYHRYKADAYLVGEGKFI 63
 QY 86 KAYLDEIIGAAKKVADAIYPGYGLSENQALRECAENGITFTGPTPEVLDLFGDKS 145
 Db 64 EAYLDEIIGTAKRHGVDAIHFGYGLSENIEFAKRCHEEGIIFTGPELEHLVMPGDKV 123
 QY 146 RAVTAAKKAGLPLVLAEST-PSKNIDDIVKSAEGQTPIFVKAVAGGSGRMRFSVSPDEL 204
 Db 124 QAREQAKANLPVPGSDGFSVSLSDVKAFAKHGHPFTIKALGGGGRGMRIVRENDV 183
 QY 205 RKLATEASREAAFGDGSVYVERAVINPOHIEVQILGDRTEGVHLYERDCSLQRRHK 264
 Db 184 QESYERAKSEAKAAGFNDVYVEKFTENPKHIEVQILADKHGNTLHLYERDCSVQRRHK 243
 QY 265 VVEIAPAOHLDELDRICADAVKCRSTGYOGAGTIVEFLVDEKGNHVIEMNPRIQVH 324
 Db 244 VVEVAVSLSDELDERICQAAQJLAENYVYVAGTIVEFLVDEGNYFIENPRIQVH 303
 QY 325 TWTEEVTEVDLVKAQMLAAGATL--KELGL-TQDKIKTHGAALOCRIPTEDPNNGFRD 381
 Db 304 TITEMVTGIDIVQSOLFADGELHCDRLGIPKQEIVCHGYAIQSRVTEPDSNGFLFD 363
 QY 382 TGTITAYRSPGAGVRLD-GAQLGGETTAHFDSDMLVWTCRGSPFETAVARAQALAEF 440
 Db 364 TGRINAYRSGGGFVGRDLRAGNFQGAIVTPYVDSLVKYSTWALTPEGAAGAAKMLRLREF 423
 QY 441 TVSGVATNIGFRLALREEDFTSKRIATGFIGDHPHLLQAPPADDEOGRILQYLDVTYN 500
 Db 424 RIRGINKITAFLENVQHRQFUSGEYNTSFIDQTPELFVFPKRKRGTKMLSFIGETIYN 483
 QY 501 KPHGVPRKDVAAPIDK--LPNIK-DLPLPRGSRDLKQGLGPAFAFARDLREQDALAVTDPT 557

Db 484 GYPCLE-KTKKPVDFKPPVKLKLSEFIPDGTQILQDQHGPEGLAKVWKQKHVLLDIT 542
 QY 558 FRAHOSLSLATRVRSTAKPAEAAVAKLTPELLSVAMGATYDVAMRFLFEDPWRDLDE 617
 Db 543 FRAHOSLSLATRVRTHDQLQIAEPTARLLPNLFSMEMWGATFDVAMRFLFEDPWRLLI 602
 QY 618 LREAMFNVINQMLLRGNTVGYTPYDSCVRAVYKAASSGVDFIRIFDADNDVDSOMRPA 677
 Db 603 LRKKAENVLFQMLLRASNAVYKNYDNLIFEDVKSANAGIDVDFRIFDSENVWEGMKLA 662
 QY 678 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYILKMAEIVKSGAHILAIDMAGLLR 737
 Db 663 IEAVGEAN-KIAETICYTGDILDSRPKYDYLAAYKKLAKLEAAGAHILGIDMAGLLK 721
 QY 738 PAAVTKLYTALRRFEDLPVHVHTDTAGGOLATYFAAQAGADAVDGCASAPLSGTTSQPS 797
 Db 722 PEAYQLVAFELKDTVTIPVHLHTDTSNGIFTYARAIEAGVDIVDVAVSSMAGLTSQPS 781
 QY 798 LSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPPESTPGPTGRVYRHEIPGGOL 857
 Db 782 ANSLYALADSESRQPNVNITALEQLAEFFWEETKRYAGFESGMNAPTEVEHEMFGQY 841
 QY 858 SNLRPAQATALGLADRELEIEDNTVAANEMLGRPTKVTPSSKVVDLALHLVAGVDPADF 917
 Db 842 SNLQQAQAKAVGLGHRNNEVKMRTYVNDMFGDVVKTPTSSKVVDMALYVNDLITEEV 901
 QY 918 AADPOKYDIPDSVIAFLRGELNPPGSGWPEPLRTRALEGRSEKAPLITEVPEEQAHLDA 977
 Db 902 YENGHLDPDSVVEFEQOLGQPYGFPKQKQIILKGRK----PITNPGENMEPIQF 957
 QY 978 DOSKER-RNSLNR-----LLEPKPTEEFLEHRRFRGNTSALDDREFFYGLVEGRE 1026
 Db 958 EAIKEELYNKLDQRVTSHDLSYALPKVMEPEFRQTFGDVSVLDTFTFFVGLRPGEE 1017
 QY 1027 TLIRLPDVTPLVRLDALISEPDDKGRNVVAVNNGQIRPMVRDRSVSVTATAEKADS 1086
 Db 1018 IEVEIDOGKT-LIVKFSISKPODDGNRIYVIFELNGQPREVLKDSKVSITSIRPKADK 1076
 QY 1087 SNKGHVAAFPAG-VVTVTVAEGDEVKAGDAVAIEAKMEATITASVDCGKIERVVVPAAT 1145
 Db 1077 SNPHIGASMPGVVYKALVEKGDVKVQGHMLTEAMKMETTVOAFDFGEVVALHVKDG 1136
 QY 1146 KVEGGDLIVVV 1156
 Db 1137 AIQTGDLILIEV 1147

RESULT 5
 F69685
 pyruvate carboxylase (EC 6.4.1.1) pycA [similarity] - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 18-Aug-2000
 C:Accession: F69685
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 A.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
 A:Authors: lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
 y, M.; Odawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
 keuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: F69685
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1148 <KUN>

Query Match	43.1%	Score	2528.5	DB 1	Length	1178			
Best local similarity	45.9%	Pred. No.	4.2e-131						
Matches	540	Conservative	187	Mismatches	415	Indels	35	Gaps	13

QY	7	GGLLKGIITLVSTHTSTSLPA-----FKKILVANRGEIAVRAAPRAALETGAA	54
DB	9	GGELLGI-----RRSTAPASPNVRRLEYKPKKVMANRGEIAIRVFRATELGIR	62
QY	55	TVAIYPREDRGSHRSFASAVRIGTEGSPVKAYLIDIDEIIGAAKYKADAITYPGYGLS	114
DB	63	TVAIYSQDQGMHRQKADAYLIGRGLAPVOAYLHIPDILIKVAKENNVDAVHPGYGLS	122
QY	115	ENAOALRECAENGITFGPTPEVLDLTGDKSRAYTAAKKAGLPVL-AESTPSKNIDILVK	173
DB	123	ERADFAGACODAGVRFGLGPEVYKMGDKVEARAIAAGVPPVPGTDAPITSLHAHE	182
QY	174	SABGQTYPIFVKAVAGGGGGRFVSPDELKRLATEASREAEAAFGDGSVYVERAVINP	233
DB	183	FSNTYGPPLIFKAAYGCGGRMVVHVSVEELEENTRAYSEALAAFGNALFVEKFIETKP	242
QY	234	QHLVEOILGDRTEGVVHLYBRDCSLQRHQKVEIAPAOHLDPDLRDRICADAVKFORSI	293
DB	243	RHIEVQLGQOYGNIILHYBRDCSIQRHQKWSIAPAAHLDPQRLTSLSDSVKLAQV	302
QY	294	GYOGAGVVEFLVDEKGNHVFIEMPRIQVETHTVEEVDLVKQAQRLAAGATLKEGL	353
DB	303	GYENAGTVVEFLVDRHGKHFIENVNSRLQVETHTVEITDVLVHAQIHVSGRSLPDLGL	362
QY	354	TQDKIKTHGAALQCRITTEPDNNGFRPDTGTITAYRSPGGAGVRLDGAQAQI-GGEITAHF	412
DB	363	RQENIRINGCAIOCRVTTEPDPAKSFQDTRIEVRSRGEGMIRLDNASAFQGAIVISPHY	422
QY	413	DSMLVKMTCRGSFPETAVARAQRALAEFTVSGVATNIGFLLRALLREDEFTSKRIATGFI	472
DB	423	DSLVLKVIYAHGKHDPAAATKMSRALAEFRVGVKNTIAFLQVNLNNQOFLAGTVDTQFID	482
QY	473	DHPHILQAPPADDEQGRILYLDVTVNKPQGVRRP-KDVAAPIDK-LPNIKDLPLPRGSR	530
DB	483	ENPELFOLRPAQNRQAQKLLHYLGHVMVNGTTPIPVKASPSPTOPVVPVAVPIGPPAGFR	542
QY	531	DRUKOLGPAAFARDLREODALAVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELL	590
DB	543	DILLREGPEGARAVRNHPGGLLLMDITFRDAHQSLLATRVKTHDLKXIAPVVAHNFSKLF	602
QY	591	SVBAWGATYDVAMRFLFEDPWRDLRELAMPNVNIQMLLRGNTVGYTYPDPSVCKRAF	650
DB	603	SMENWGGATEDVAMRFLFYECPPWRRLQELRELIPNIPFQMLLRGANAVGNTYNPDPNVFKF	662
QY	651	VKEAASGGVDIFRLEDALNDVQMRPAIDAVLENTAVAEVAMAYSGDLSDPNEKLTYLD	710
DB	663	CEVAKENGMDVFRVFDSENLPLNMLLMEAGSAG-GVVEAAISYTGVDADPSRTKYSLQ	721
QY	711	YLLKMAEEIVKSGAHILAIKDMAGLLRPAAVTKLVATLRREF-DLPVHVTHDTHAGOLA	769
DB	722	YVYGLAEELVRAGTHILCIKDMAGLLKPTACTMLVSSLRORFPDPLPHIHTHDSGAGVA	781
QY	770	TYFAAQAGADAVDASAPISGTTSQPSLSAIVAAFAHTRDRTGLSLEAVSDLEPYWEAV	829
DB	782	AMLCACAGADVDVADSMGNTSOPSMGLVACTRGTPDLDTVPMPFRVFDYSEWEGA	841
QY	830	RGLYLPPESTCPGPTGR-VYRHEIPGSGLSNLRQAQATGLADREFELIEDNYAAVNEML	887
DB	842	RGLYAAFDCTATMKSGNSDVENEIPGGQYTNLHFQAHSMGLGSKFKEVKKAVVEANQML	901
QY	888	GRPTKVTTPSSKVGDDLALHLVGADVPDAFPAQDPQKYDIPDSYTAETLRGELGNPPGGWPE	947
DB	902	GDLIKVTTPSSKIVGDLAQFVQVQNGLSRAEAAQAEELSFPSSVVEFLQGYIVPHGCGFPE	961
QY	948	PLRTRAL-----EGRSEGAPLTEVPEEQAHLDA-DDSKERNRNSLNRLFLPKPTEEFL	1000
DB	962	PFKSKVLKDLPRVEGRPGSLPLDLQALBKELVDRHEEVTPEEDVLISAAMYDPVFAHFK	1021

Qy 1001 EHRRFNTGALDDREFPYGLVREGREFLIRLPDVRTPLLVRLDAISPDPDGMRNVAVY 1060
Db :
Db 1022 DFTATFGPLDSLNRFLQGPKTAEEVELEGRKT-LHIKALAVALSLNRAQGQVFEL 1080
Qy 1061 NGQIRPMRVDRSVESYTATAEKADSSNKGHVAAPAG-VVTYTVAAEGDEVKAGDAVAIL 1119
Db :
Db 1081 NGQURSLVKDTQAMKEHMFHPKALKDVKGQIGAPMPGKVLDIKVVAGAKVAGQPCLCVL 1140
Qy 1120 EAMKEEATITASVDGKIERYVVPAAATKVEGGDLIVVV 1156
Db :
Db 1141 SAMKMETVVTSPMEGTVRKRVHTKDMTEGGDLLILEI 1177

RESULT 7
AH1208
pyruvate carboxylase homolog pycA [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AH1208
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
. : Dominguez-Bernal, K.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A::Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1208
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1146 <LA>
A:Cross-references: GB:NC_003210; PIDN:CAC99150.1; PID:g16410474; GSPDB:GNU0177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: pycA
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bindin

Query Match 42.58; Score 2494; DB 2; Length 1146;
Best Local Similarity 45.74; Pred. No. 3.2e-129;
Matches 525; Conservative 186; Mismatches 408; Indels 30; Gaps 11;

Qy 30 KKILVANRGETAIVRAFRALLETGAATVAIYPREDRSGFSHRSFASEAVRIGTEGSPVKAYL 89
Db :
Db 5 KKVILVANRGETAIVRMRACTELKIKTVIAYSQEDTGSFHFKSDAEAYLVGAGKKPIDAYL 64
Qy 90 DIDETIGAANKVADAILYGYGFSELNAQLARECAENGITFIGPTPEVLDTLGDKSRVIT 149
Db :
Db 65 DIENIIIAKESGADAIHPGYGSELSENIIEFARCEQEGIIFFVGPKSHLDMFDGIKAKE 124
Qy 150 AAKKAGLPVLAEST-PSKNIDDIIVKSAEQGTPIFYKAVAGGGGGRMRFSSPDELKLKA 208
Db :
Db 125 QALLADIPIVPGNGPVAGIKVEEFGEKNKYPLMIKASUGGGGGRMVVESKEHVKESEF 184
Qy 209 TEASREAFAFGDSVYVERAVINPOHIEVIQLGDRDTGEVHLHYERDCSLQRHQKWVET 268
Db :
Db 185 ERASSERAFAFNDEYVVEKVMNPRHIEVIQLGDTGNIVHLFERDCSIQRHQKVEV 244
Qy 269 APAQHLDPELRICADAVKFCRSIGYGAGTVFEFLVDEKGNHFVTEMNPRIQVEHTVTE 328
Db :
Db 245 APCNAITSETLNRNICDAAVKLMKNVDYINAGTVEFLV-EGDDPFYTEVNPVQVEHTITE 303
Qy 329 EVTEVDLVRAQMFLAAGATILKELGLI---QDKLTHGAALOCRTITDDPNNGFRPDGTGI 385
Db :
Db 304 MITGDIVQSLEFIADGYALHDQLVAIPKQEDIHINGSIAIQSRITTEDPLNNFMPTGKV 363
Qy 386 TAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDSETAVARAQRALAEFTVSG 444
Db :
Db 364 DTYSTGGGVRLDAGNGFGQTWTTFYDLSLLVKLTWGTTEQATRKMRNLIERING 423
Qy 445 VAFNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAAPPADDQGGRLDYLDADVTKNPHG 504
Db :
Db 424 VKTNIFELLNVNRPDFAGSNVTSFIDTPELFKPPHTRDRGTKTLRYIGNVTVNGPFG 483

Db 1017 ELBKGI-LIKLNSIGEPTADTRIVYFELNQPREINQDMNVOSTVIARRKIDITNP 1075
 QY 1090 GHVAAPFAG-VVTVTVVAEGDKAGDAVAIIIEAMKEATITAGSDGKIERVVVPAATKVE 1148
 Db 1076 EHVCAWTGVSIOVVVKGDSVAKGDBLLITTEAMKMETTIOAPFDEGVSSIIYSDGDTIE 1135
 QY 1149 GGLIIVVVS 1157
 Db 1136 SGDLLEVN 1144

RESULT 9
 D97227
 Pyruvate carboxylase, PYKA [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
 C:Accession: D97227
 R:Noelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Dally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: D97227
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1144 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK80607.1; PID:g15025689; GSPDB:GNC0168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC2660
 C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 42.5%; Score 2490.5; DB 2; Length 1144;
 Best Local Similarity 45.2%; Pred. No. 5e-129;
 Matches 519; Conservative 204; Mismatches 392; Indels 33; Gaps 14;

QY 29 EKKILVANGETAVRAFAALETGAATVAIYFREDGSRHSFASAVRIGTSGPVKAY 88
 Db 5 FAKVLVANGETAIFRACHBELGINTVAIYSEEDKLALFRKADESILIGQNKGPVAY 64
 QY 89 LDIDEIIGAIAKVKADAIYPGGLFSENAQALCAEAGTITFIPPTPELDLTDKSRV 148
 Db 65 LNIDEIINLALKGVDAIHGPGGLFSESESRCTEAGIEFIPGDMMDKLIGDKINSK 124
 QY 149 TAAKAGLVL-AESTPSKNIDDIYKSAEGQTYPIFVKAVAGGGGRMFVSPDELRKL 207
 Db 125 LAAKAAGVKTIPGVKEPIETEQQAIEFARTCGYPVMVKAAGGGGRMRIVEKEEDLIAA 184
 QY 208 ATEASREAAFGDGSVVYVERAVINPOHTEVOILGDRTEGVVHLYERDCSLORRHQKVE 267
 Db 185 CSRSAKKAATGIEDIFIEKLEGPKHIEVQVLGDKYGNIVHLYERDCSVORRHQKVE 244
 QY 268 IAPAQHLDELDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFIEENPRIQVEHTVT 327
 Db 245 LTPAVMSSEKRLCEICEDALKIARSIGYSAGTLELLDKHGNHVFIEENPRVQVEHTIT 304
 QY 328 EETVEVDLVKAMRLAAGATLK--ELGL-TQDKIKTHGAALOCRIITPEDPNNGFRPDGT 384
 Db 305 EMVTGIDIVQSQILIAEGYKLNSPEVGINSDIEHVNGVIAIQCRITTEDPSNFAPDCK 364
 QY 385 ITAYRSPGAGVRLDGA-AQLGGEITAHEDSMIVKTCRGSDFETAVARAQALAEFTVS 443
 Db 365 IDVYRTGSGFGLRDGGNGFTGAVISPYDLSLVKSTSWSRFTFEDAIRKAIKAITETYS 424
 QY 444 GVATNIGFLRALLREDEFTSKRIATGFIGDHPHILQAPPADDEQGRILDYADVTWVKPH 503
 Db 425 GVKTNIDFLINLVNHNHETFRKGLCDNFIANNEPELFEITPRIDTELVLKFEIKVYVNEHT 484
 QY 504 GVRPKDVAAPIDKLP--NTKDLPLRGSBRDLKQLGPAFAADRLREQDALAVTDTTFRDA 561
 Db 485 GHK---IEVDVPSVPKYEIKE-PL-RGTQILDEKGPGLVEWIKDQDKLLLTDTTMRDA 539

QY 562 HQSLLATRVRSFALKPAFAEAVAKLTPELLSVEAWGATYDVAMRFLFEDPWRDLRELA 621
 Db 540 HQSLMATELRTVDMVKIAAESVLAKDLFSWMGAGTPTDPTAYRFLKESPEWERLERLKR 599
 QY 622 MPNVNTQMLLRGNTVGYTPYDSCVCAEAFKEAAGSVDIFRIFDALNDVQMRPAIDAV 681
 Db 600 VPNVLFQMLRGANAVGYKNYPDNVIREFKOSKSGIDVFRIFDLSLNVYKMGNEVAIDEV 659
 QY 682 LETNTAVAEVAMAYSGDLSDPNEKLYTLDYILKMAEEIVKSGAHILAIKDMGLLRPAV 741
 Db 660 LNOG-KVAECACMYTGDILDTNRDKYTLNYYVNLAKIEKSGAHILIGIKDMSALLPYAA 718
 QY 742 TKLVTLALRRFEDLPVHVHTHTAGGATYFAAQAQADAVDQASAPLSTTTSQPSLSAI 801
 Db 719 LKLIRALKNEISIPILHHTHTDTTNGVATVMAAHAGVDIADTAFNMSGTSLTSPALNSV 778
 QY 802 VAAFAHTRDGTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGQSLNLR 861
 Db 779 VAALKNTDRDMDIGDLQKISDYWTVRPVYSKFESGLKAVSAEIKYKIEPGGOYSNLK 838
 QY 862 AQATALGLADRFELIEDNYAANEMGRPTKVTTPSSKVVGVGLALHLVAGAGVDPADPAADP 921
 Db 839 PQVESGGLHREPEQVKEMYREYNIMLGDIVKTPSSKNVGDALAFMVQNELTSENILEKA 898
 QY 922 QXYDIPDSVIAFLRGLGNPPGGWPEPLRTRALEGSEKAPLTFEYPEREQALHDADDK 981
 Db 899 KDMPPDPSVSVYFKGMGQPKGGFPKELQIVL---KDEEATCTCPGELLDPDEDFDKIR 954
 QY 982 ERENSLNRL-----LFPKPTPEELEHRRREGNTSALDDREFFVGLYEGRETLIR 1030
 Db 955 VRLKENKLEPTDKOVISYALYDPVDFEYLKYNKYEDLSRMGSDVFFHGLABGEISELE 1014
 QY 1031 LPDVRTPLLVRDLDAISEPDDKMRNVVANNVGQIRPMVRDRSVESVATAEK---ADSS 1087
 Db 1015 IAEGKT-LVQLLHGLKDKQGNRTLVEFVNGNRREIKIKDKVSSKSEIVEIEVIADSS 1073
 QY 1088 NKGHVAAPFAG-VVTVTVVAEGDEVKAGDAVAIIIEAMKEATITASVDGKIERYVVVPAATK 1146
 Db 1074 NKEIGASIPGNVYKVFVPGDKVKKGSGLMVIEMKMETNVSVDGTVGGIFVKEGQ 1133
 QY 1147 VEGGDLIV 1154
 Db 1134 VQSGQLIV 1141

RESULT 10
 G89881
 Pyruvate carboxylase [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: G89881
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
 ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: G89881
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1150 <KUP>
 A:Cross-references: GB:BA000018; PID:g13700915; PIDN:BAB42211.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: pyca
 C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bindi

Query Match 42.4%; Score 2489; DB 2; Length 1150;
 Best Local Similarity 45.2%; Pred. No. 6.1e-129;
 Matches 527; Conservative 193; Mismatches 383; Indels 62; Gaps 14;

QY 30 KKLIVANGETAVRAFAALETGAATVAIYFREDGSRHSFASAVRIGTSGPVKAYL 89

Db 5 KULVANRGEIAIRIFRAAAELDSTVIALYSNEDKSSLHRYKADESYLVGSDLGPAESYL 64
QY 90 DIDEIGAAKKVADALPYGVGFLSENAOLARECAENGITFIPTPEVLDLTGDKSRAVT 149
Db 65 NIERIDVAQANVDALHPGIGFLSENEQFARRCAEEGIFGPHLEHDMFGDKVART 124
QY 150 AAKKAGLPVL-AESTPSKNIDDDIVKSAEGOTYPIFVKAVAGGGGGRGMFVSSDPDELKLA 208
Db 125 TAIKADLPVPGTDGPIKSVELAKEFAEEAGFPIMIKATSGGGKGNRIVRESELEDAF 184
QY 209 TEASREAEAFGDSVYVERAVINPQHIEVQIILGDRTEGVHLYERDCSLQRHQKVEI 268
Db 185 HRAKSEAEFGSEVSEYIERIDNPKHIEVQIVQIGDEHGNIVHLFERDCSVQRHQKVEV 244
QY 269 APAQHLDPFLDRICADAVKFCRSIGYOGAGTVEELV--DEKGNHVFIEMNPRIOVEHTV 326
Db 245 APSVGLSPTLRICDAAIQIMENIKVYNAGTVEFLVSGDE---FFIEVNPVRQVSHHTI 301
QY 327 TEEVTEVDLVKAQMLAAGAIL--KELGLTQDK--IKTHGAALQCRITTEDPNNGFRPDTG 383
Db 302 TENVTGIDIVKTOQLVAAAGADLFGEIINMPQOKDITTLGVAIQCRITTEDPNDFMPDTG 361
QY 384 TIATSPGAGVRLD-GAQLGSEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTV 442
Db 362 TIATSSGGFVRLDAGDGFQGAETSPYDYSLLVLSLTHAIFKQAEKRVSLREMRI 421
QY 443 SGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEOQGRILDYLAADVTKNP 502
Db 422 RGVKTNIPFLINVMKKNKFTSGDYTKFIEETPELFDIQPSLORGTLEYIGNVIN-- 479
QY 503 HGVRPDVAAPIDKLPNIKDLPLP-----RGSRLRLKQLGPAAPFARD 544
Db 480 -----GFPNVEKRPPDYELASIPTVSSSKIASFSGTQKLLDEVGPKGVAEW 526
QY 545 LREQDALAVTDTTFRDHAQSLATRVKSPALKPAEAAVAKLTPELLSVKAWGATVDVAM 604
Db 527 VKQDDVLLTDTTFRDHAQSLATRVTKDMINIAKSTADVDFDKGFSLEMMGATEDVAY 586
QY 605 RFLFEDPWRDLDELREAMPNVTOMLLRGNTVGYTPYDPSVCRAFKVKEAASGVDFIRI 664
Db 587 NFLKENPWERLERKRAIPNLFQMLLRASNNAVGYKNYPDNVTHKFVQESAKAGIDVRI 646
QY 665 EDALNDVQMRPAIDAVLENTAVAEVAMAYSGLSDP-NEKLYTIDYILKMAEEIVKSG 723
Db 647 FDSINVMQMKVANEAVQAG-KISEGTICYTGDIILNPKERSNTYILEYVVKLAKELEREG 705
QY 724 AHILAIDKAGLRLPAAVTKLVTLARRREFDLPHVHTHTDAGGOLATYFAAAAGADAVD 763
Db 706 FHILAIDKAGLRLPAAVTKLVTLARRREFDLPHVHTHTDAGGOLATYFAAAAGADAVD 765
QY 784 GASAPLSGTTSPQSLSAIIVAFAHTRDRTGLSLEAVSDLEPYWEAVRGLYLPESGTPG 843
Db 766 TAVASMSGLTSPANSLSYALNGFPRHRTDIEGMESLSHYWSTVRYTSDFESDIKSP 825
QY 844 TGVYRHEIPGGSLNLAQAATGALGLADRFELIEDNYAAVNEMLGPTKVITSSKVGDL 903
Db 826 NTEIYQHEMPGGQYSLNSQAQSLGGERFDEVKMDYRKRVNLFGLDIVKVTSSKVGDM 885
QY 904 ALHLVAGVDPADFAADPOKYPIDIPDSVIAFLRGLNPGPGWPEPLRTRALEGRSEKAP 963
Db 886 ALYVMQNLDQESVITDGYKIDFPESVSVFKEIGQIPVNGFNKDLQAVILKQOE---A 941
QY 964 LLEVPEEQAHLDADDSKE-----RNSLNRLFPKPTPEFFLEHRRFRFGTSAL 1012
Db 942 LTARPEYLEPVDPEKVRLELLEEEQGPVTEQDIISYLVPKVYEQYIQTRNQYGNLSLL 1001
QY 1013 DOREFYGVLEGETLIRLPDVTPLLVRLDAISEPDDKGMNVANVNGQIRPMVRDR 1072
Db 1002 DPTPTFFGMNGETVEIET-DKGKRLIIKLETISEDENGNRTIYAMNGQARRIYKDE 1060
QY 1073 SVESVTATAEKADSSNKGHVAAPFAGVVT-VVVAEGDEVKAGDAVAILEAKMEATITAS 1131
Db 1061 NVHTNANVKKADKSNPISHIQAMPGSVTEKVSGETVKANQPLITEAMKMETIQAP 1120

QY 1132 VDGKIERVVVPAAKVVEGGDLIVVV 1156
Db 1121 FDGVIKOTVWNGTDITATGDLLEI 1145

RESULT 11

AE2911
Pyruvate carboxylase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AE2911
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo-
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavich, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kan
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE2911
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1174 <KUR>
A:Cross-references: GB:AE008688; PIDN:AAL43707.1; PID:g17741236; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: pycA
A:Map position: circular chromosome
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bindi

Query Match 42.2%; Score 2474.5; DB 2; Length 1174;
Best Local Similarity 46.5%; Pred. No. 3.9e-128;
Matches 540; Conservative 174; Mismatches 406; Indels 41; Gaps 19;
QY 25 TLPAFKILVANRGEIAVRAAFRAALETGAATVAIYIPREDRSGFHSFASAVRIG----- 79
Db 20 TVLKISKILVANRSEIAIRVRAANEIGIKTVAIWAEDKLSLHRKADSEYQVGRGPHL 79
QY 80 -TEGSPVAKYLDDEIIGAIAKKVADAIYPGYGLFSENAGLARECAENGITFIPTPEVL 138
Db 80 AKDMGPIESYLSIEEIVRAKLSGADAIHPGIGLSESEPEFVEACNKAAGITFIPTPTDM 139
QY 139 DLTGDKSRVATAAKAGLPVLAESTP-SKNIDDIVKSAEGOTYPIFVKAVAGGGGRGMF 197
Db 140 RQLGNKVAARNLAISVDVPPVVPATNPLPDIAEVEKAEIEGYPVMLKASWGGGGMRA 199
QY 198 VSSPDELKRLATPAEAREAAFGDGGVYVERAVINPQHIEVQIILGDRTEGVHLYERDCS 257
Db 200 IRKKEDLAREVTEAKREAAAFKGVLEKLVKVERARHVESQILGDTGHNHVFLEDCS 259
QY 258 LQRRHOKVVEIAPAHLDPFLDRICADAVKFCRSIGYOGAGTVEELV-EKGNHVFIE 316
Db 260 IQRNKVVVERAPAPYLSAQRLAAYSLKIAAATNYIGAGTVEIMADTKFYFIEV 319
QY 317 NPRIQVHEVTVEEVEVDLVKAQMLAAGAIL--KELGL-TQDKIKTHGAALQCRITTED 373
Db 320 NPRIQVHEVTVEVTGIDIVKQIHLEGAAGTAESEGVKQEDIRLNGHALQCRITTED 379
QY 374 PNNGFRPDTGTTATYRSPGGAGVRLD-GAQLGSEITAHFDSMLVKMTCRGSDFETAVAR 432
Db 380 PEHNFIPDYGRITATYRSASGFIRLDGGTSYTGAVITRYDPLLVKVTAWAPEDEAISR 439
QY 433 AGRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEOGRILD 492
Db 440 MDRLNREFIRGVATNLITELALIGHDSFRNTYITRFDISTPELFAQVKRQDRATKLLT 499
QY 493 YLADVTN---KPHG-VRPKDVA--PIDKLPNIKPLPRGSRORLKLQGPAAFAADLRE 547
Db 500 YLADVTNNGHPETKGRAPDAKAAKPI--VPYI-DAPTDTGKQLDLKLGPGFADWNRN 556
QY 548 QDALAVTDTTFRDHAQSLATRVKSPALKPAEAAVAKLTPELLSVKAWGATVDVAMREL 607

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Db 557 EKRVLVDTTMRDGHOSLLATVRVTHDIARVASVTSKALPQLLSLECGWGAFTDYSMRFL 616
QY 608 FEDPWRDLDELREAMPNNVNIQMLRGRNTVGYTPYDPSVCRFAVKEAASSGVDFIRIFDA 667
Db 617 TEDPWERLSLIREGAPNLQMLLRGANGVGYKNYPDNVVKYFVQAARGVDLFRVDC 676
QY 668 LNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDFNEKLYTLDDYLLKMAEETVKSAGHIL 727
Db 677 LNWENMRVMSMDATAEEN-KICEATICTYDGLLSARPKYDLKYTYNLAVELEKAGAHII 735
QY 728 AIKDMAGLLRPAAVTKLVTRREFDLPHVHTHTAGSGLATYFAAAQAGADAVDGASA 787
Db 736 AVKDMAGLLKPAKAAKLVKALREATGLPIHFHTDTSGLSAATVLAADVADAGVDAAMD 795
QY 788 PLSGTTSOPSLSAIWAFAHTRRDGLSLEAVSDLEPYWEAVRGLYLPFESGTPGTRGV 847
Db 796 AFSGNTSOPCLGSIVEALSGSERDGLDTEWIRISFYWEAVRNOYAAAFESDLKGPASEV 855
QY 848 YRHEIPGQSLNLRQAATAGLADREFELIEDNYAAVNEMLGRPTKVTPSSKVVGDALHL 907
Db 856 YLHEMPGGQFTNLKEQARSGLSEHWEVAQAYADANRMFGDIVKVTPESSKVVGDALMM 915
QY 908 VGAGVDPADFAADPOKYIPDPSVIAFLRGLGNPPGWPPELURTRALEGRSEGKAPLTV 967
Db 916 VSQDLTVADVENPREVSEFSDPSVSMKGLDGLQSGPGWPEALQKAL-----KGEKPYTVR 971
QY 968 PEE--EQAHLDDADDKERRNSLNR-----LLFPKPTPEEFLEHRRRFGNTSALDDR 1015
Db 972 PGSLEEDADLDA-ERKVIETKLERKVDDEFASVLMYKPVETDFALTAEITYGPSVLP 1030
QY 1016 EFFYGLVEGRETLLRPLDVRTPPLVLRDAISEPDDKGMNRNVANVNGQIRPMRVRDRS-V 1074
Db 1031 AYFYGMEDGEELEFADIERGKTLIVN-QASSGIDDKGMVTVPFPEINGOPRIKVPDRAHG 1089
QY 1075 ESVTATKADSSNKHGVAAPFAGVVT-VTVAEGDEVKAGDAVAIIIEAMKMEATITASVD 1133
Db 1090 ASGSAVRRKAPGNASHIGAPMPGVISRVFINQGEVKAGDVLISIAMKMETALHAERD 1149
QY 1134 GKIERVVVPAATKVEGGDLIV 1154
Db 1150 GKIAEVLVKGQDQIDAKDLII 1170

RESULT 12
C97686
pyruvate carboxylase (U51439) [imported] - Agrobacterium tumefaciens (strain C58, Cereon
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: C97686
A.: Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorillo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: C97686
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1174 <KUR>
A:Cross-references: GB:AE007869; PTDN:AAK88444.1; PID:gl5157941; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C4940
A:Map position: circular chromosome
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 42.2%; Score 2474.5; DB 2; Length 1174;
Best Local Similarity 46.5%; Pred. No. 3.9e-128;
Matches 540; Conservative 174; Mismatches 406; Indels 41; Gaps 19;

QY 25 TLPAFKKTLVANRGEIAVRAPRALETCAAVVAIYPREDRGSFHRSEFASAVRIG----- 79
Db 20 TVLKISKTLVANRGEIAVRAPRALETCAAVVAIYPREDRGSFHRSEFASAVRIG----- 79
QY 80 -TEGSPVKAYLDDIIDEIIGAARKKADAIYPGYGLFSENQAQLARECAENGITFIGTPPEVL 138

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Db 80 AKDMGPIESYLSEIEVIRVAKLSGADAIHPGYGLLSESPFEVACNKAIGITEIGTPDPM 139
QY 139 DLTGKDSRAVTAAKKAGLPVLAESTP-SKNIDDIIVKSAAGQYPIFVKAAGGGGRGFRF 197
Db 140 ROLGNKVAARNIAISVDVVPATNPLPDIDIAEVEERMAEEIGYPVMLKASWGSGGGMRA 199
QY 198 VSSPDELKRLATFEASREAEAFGDSVTVVERAVINPQHIEVQILGDRTEVHVHLERDCS 257
Db 200 IRKKEDLAREYTEAKREAAFGKDEVLEKLEVARHVESQILGTHGNVVHLERDCS 259
QY 258 LORRHQKVVEIAPAOHLDELDRICADAVKFCRSIGYQAGTVEFLVD-EKGNHVFIRM 316
Db 260 IORRNQKVVERAPAPYLSQAQRLAAAYSLKATAATNYIGAGTYEVLMDADTKGYFTFV 319
QY 317 NPRIQVHTVTEVEVDLVKAQMLAAGATL--KELGL-TQDKTKTHGAALQCRITTED 373
Db 320 NPRIQVHTVTEVTGIDIVKQIHLLEGAAIGTAESGVKQEDIRLNGHALQCRITTED 379
QY 374 PNNGFRPDGTITAYRSPGAGVRIL-DGAAQLGGEITAEHDSMLVKMTCRGSDFETAVAR 432
Db 380 PEHNFIPDYGRITAYRSASGFGIRLDGGTSYTGAVITRYDPLLVKVTAWAPEDEALSR 439
QY 433 AQRLALETVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEGRILD 492
Db 440 MDRLREFRIIRGVATNLTFLEAIIIGHDSFRNNYITRTFIDSTPELFAQVKKQDRATKLIT 499
QY 493 YLADVTVN---KPHG-VRPKDVA--PIDKLPNIKDLPLPGSRDRRLKOLGPAAPARDLRE 547
Db 500 YLADVTVNGHETKRAKAPDAKAAKPI--VPYI-DAPIDPDGKQLDGLKPGFADWNRN 556
QY 548 QDALAVDTTFRDAHOSLLATVRVTSFALKPAEAAVAKLTPELLSVEAGGATYDVAMRFL 607
Db 557 EKRVLVDTTMRDGHOSLLATVRVTHDIARVASVTSKALPQLLSLECGWGAFTDYSMRFL 616
QY 608 FEDPWRDLDELREAMPNNVNIQMLRGRNTVGYTPYDPSVCRFAVKEAASSGVDFIRIFDA 667
Db 617 TEDPWERLSLIREGAPNLQMLLRGANGVGYKNYPDNVVKYFVQAARGVDLFRVDC 676
QY 668 LNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDFNEKLYTLDDYLLKMAEETVKSAGHIL 727
Db 677 LNWENMRVMSMDATAEEN-KICEATICTYDGLLSARPKYDLKYTYNLAVELEKAGAHII 735
QY 728 AIKDMAGLLRPAAVTKLVTRREFDLPHVHTHTAGSGLATYFAAAQAGADAVDGASA 787
Db 736 AVKDMAGLLKPAKAAKLVKALREATGLPIHFHTDTSGLSAATVLAADVADAGVDAAMD 795
QY 788 PLSGTTSOPSLSAIWAFAHTRRDGLSLEAVSDLEPYWEAVRGLYLPFESGTPGTRGV 847
Db 796 AFSGNTSOPCLGSIVEALSGSERDGLDTEWIRISFYWEAVRNOYAAAFESDLKGPASEV 855
QY 848 YRHEIPGQSLNLRQAATAGLADREFELIEDNYAAVNEMLGRPTKVTPSSKVVGDALHL 907
Db 856 YLHEMPGGQFTNLKEQARSGLSEHWEVAQAYADANRMFGDIVKVTPESSKVVGDALMM 915
QY 908 VGAGVDPADFAADPOKYIPDPSVIAFLRGLGNPPGWPPELURTRALEGRSEGKAPLTV 967
Db 916 VSQDLTVADVENPREVSEFSDPSVSMKGLDGLQSGPGWPEALQKAL-----KGEKPYTVR 971
QY 968 PEE--EQAHLDDADDKERRNSLNR-----LLFPKPTPEEFLEHRRRFGNTSALDDR 1015
Db 972 PGSLEEDADLDA-ERKVIETKLERKVDDEFASVLMYKPVETDFALTAEITYGPSVLP 1030
QY 1016 EFFYGLVEGRETLLRPLDVRTPPLVLRDAISEPDDKGMNRNVANVNGQIRPMRVRDRS-V 1074
Db 1031 AYFYGMEDGEELEFADIERGKTLIVN-QASSGIDDKGMVTVPFPEINGOPRIKVPDRAHG 1089
QY 1075 ESVTATKADSSNKHGVAAPFAGVVT-VTVAEGDEVKAGDAVAIIIEAMKMEATITASVD 1133
Db 1090 ASGSAVRRKAPGNASHIGAPMPGVISRVFINQGEVKAGDVLISIAMKMETALHAERD 1149
QY 1134 GKIERVVVPAATKVEGGDLIV 1154

```


Db 1150 GKIAEVLVKGPDQIDAKDLII 1170

RESULT 13
AE3285
pyruvate carboxylase (EC 6.4.1.1) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C:Accession: AE3285
R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AE3285
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1158 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL51448.1; PID:gl7982157; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0266
A:Map position: I
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
C:Keywords: ligase

Query Match 42.0%; Score 2465.5; DB 2; Length 1158;
Best Local Similarity 46.5%; Pred. No. 1.2e-127;
Matches 537; Conservative 172; Mismatches 408; Indels 37; Gaps 15;

QY 31 KILVANGETAVAFRAALETGAATVAIYPRDRGSGHRSFASAVRIG-----TEGSP 84
Db 10 KILVANKESEIAIRVFAAANGLKTVTIWAEEKLSLHFRKADESYQVGRGPHLDRLGP 69
QY 85 KYAYLIDITIGAAKKVADAIYVGYGFLSENAQLARECAENGITIGTPPEVLDLTGDK 144
Db 70 IEYSLSIDETIRVAKLSGADAIHPGYLLSESEFEFAACAENGIVFGRKPTMRRLGN 129
QY 145 SRAVTAACKAGLPVLAESTP-SKNIDDIYKASAGQTYPIFVKAVAGGGGMRGVFVSSPDE 203
Db 130 VAARNLAIEIGVVPVATDPLPDMDDEVKKLAQIGYPLMLKASWGGGGRMRAIAREAD 189
QY 204 LRKLATEASREAAFGDSVYVERAVINPOHTEVOILGDRTEGVVHLVYEROCGLQRHQ 263
Db 190 LAHEVMEAKREAAFGKDEKLEKVERARHVEVQILGDTYGNVHVFELFEROCGIORRNQ 249
QY 264 KYVEIAPAOHLDELDRICADAVKFCRSIGYOGAGTVEFLVD-EKGNHVFTEMNRIQV 322
Db 250 KYVERAPAPYLNDAQRRELADYGLKTAHATDYIGAGTVEFLMDATGKFFYEVNPRIOV 309
QY 323 EHTVTEEVTEVDLVKQMLAAGATL--KELGL-TQDKIKTHGAALQCRITTEDPNNRFR 379
Db 310 EHTVTEEVGIDIVKQAHILEGFAIGTPEGVPRQEDIRLNGHALQCRITTEDPQNF 369
QY 380 PDTGTTIAYRSGGAGVRLD-GAAQLGGETTAHFDSMLVKMTCRGSDFTAVARAORALA 438
Db 370 PDYGRIOATRSAGGIRLDGGTAYSGAFITRYDPLLVKYVATSGATPLEATHRMDRALR 429
QY 439 EFTVSGVATNIGFLRALLREEDFTSKRIATGFTGDPHPLLQAPPADDEQGRILLADYV 498
Db 430 EFRIRGVATNLIFLEAIINHPFLSNDYTRITDTTPELFQMKRQDRATKLLTYTADYV 489
QY 499 VN-----KPHGVKPKDVAAPIDKLPNIKDLPLPRGSRDLKOLGPAFAARDLREODALAV 553
Db 490 VNGHPETKGRAPARDAAPK--RVPMFGDKLVADGTFKQLLDQLGPKKFAENMRNEKRALI 547
QY 554 TDTTFDASHOSLATAVRFSALKPAAEAVALKLTPELLSVBANGGATYDVAMRFLFEDPDW 613
Db 548 TDTTMRDGHOSLATAVRDYDARTANAYAAQALPNLFSLCWCWGATFDYSMRFLTBDPWE 607
QY 614 RLDELREAMPVNIOMLLRGRNTVGYTPYDPSVCFRAVKEAASSGVVDIFRIFDALNDVQS 673
Db 608 RLALYREGAPNLLQLMLRGANGCVGKYSYPDNVVVFVREARAGIDLFRVFDLSLNWEN 667

QY 674 MRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYLLKMAEEIVKSGAHILAIKDMA 733
Db 668 MRVSMADVLEEN-KLCEAAICYTGDIILNPRKAYDNLNYVNLAKVEKAGAHITIAVKDMA 726
QY 734 GLLRPAAVTKLVTRRREFDLPVHVHTDHTAGGOLATVFAAAQAGADAVDGASAPLSGTT 793
Db 727 GLLKPAARVLFKALRETDLPFIHFHTDHTSGISAANVLAIDAGVDVDAAMDALSGNT 786
QY 794 SQSLSIAVAAFAHTRDRTGLSLEAVSDLEPPYWEAVRGLXLPFFESGTPGTRVYRHEIP 853
Db 787 SQPLGSGIVFALHGSERDSGLDPLIRRIISFYWEAVRHOYAAAFESDLKGPASEVYLHEMP 846
QY 854 GGOLSNLRQAATGALGADRELELDNVAANVEMLRGRTKVTTPSSKVGDLALHLVGAVD 913
Db 847 GGQFTNLKEQARSGLGLETRHVEVAAQADVNRMGDIIVKVTSPSKVGGDMALMVAODLT 906
QY 914 PADFAADPPQKIDIPDSVIAFLRGLGELNPPGGWPEPLRTRALEGRSEKAPLITEVPEE--E 971
Db 907 VADVENPAKDIAFPDSVSVMMRGDLGQPPSGWPEALQKVL---KDEKPTVVRPGSLLP 962
QY 972 QAHLDA-----DUSKERNSS-----LNRLLPKPTTEELEHRRRFGNTSALDDREFFGLV 1022
Db 963 AADLDAERKSFEDSVGRKLSQDBFASALMYPKVTIDYATAHETYGPTSVLPTVPYFYGLK 1022
QY 1023 EGRETLRLPLDVRTEPLLVRDLDAISEPDDKGMNVVANVNGOIRPMRVDRDSVESVTATAE 1082
Db 1023 PEEVFDLGERGKTLIVN-OAMSETDEKGMVTVFFELNGOPRRKIKVFNRAKASGSGVRR 1081
QY 1083 KADSSKNHGVAAPFAGVY-TVTVAEGDEVKAGDAVAITIEAMKEAITTASVDGKIERYVV 1141
Db 1082 KVEAGNDKQVAGPMPGVISTVAVVAGQVGTQGVLLSIEAMKMETAIHAERDGTIARVLV 1141
QY 1142 PAATKVEGGDLIVV 1155
Db 1142 RPGEQIDAKDLII 1155

RESULT 14
T20346
pyruvate carboxylase (EC 6.4.1.1) D2023.2 [similarity] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
C:Accession: T20346
R:Kershaw, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19260
A:Accession: T20346
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1175 <WIL>
A:Cross-references: EMBL:Z81052; PIDN:CAB02872.1; GSPDB:GN00023; CESP:D2023.2
A:Experimental source: clone D2023
C:Genetics:
A:Gene: CESP:D2023.2
A:Map position: 5
A:Introns: 34/3; 103/3; 246/1; 451/3; 567/2; 821/1; 1045/3; 1126/3
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
C:Keywords: ligase
F:1140/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 42.0%; Score 2461; DB 2; Length 1175;
Best Local Similarity 45.1%; Pred. No. 2.2e-127;
Matches 522; Conservative 201; Mismatches 389; Indels 46; Gaps 14;

QY 29 FKKILVANGETAVAFRAALETGAATVAIYPRDRGSGHRSFASAVRIGTEGSPVAY 88
Db 32 FKNVMVANGETAIRVFRALTEINLTNSVAIYAEQDKNSMHLKADAEAYLVGKGLPVAAY 91
QY 89 LDIDETIGAAKKVADAIYVGYGFLSENAQLARECAENGITIGTPPEVLDLTGDKSRV 148
Db 92 LTIDQIETALKHNIDAIHPGYGFLUSERSDFAAACQAGIVFTGSPDVMARWGDKVAAR 151

149 TAAKKAGLPLVABST-PSKNIDDIVSAEQTYPIFVAVAGGGGMRFFVSPDELRLK 207
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
152 AATAEAGVVPVPGTPIITADRAVEFAKQYGPPIILKAAAGGGGRIIRVVDKLEVEEA 211
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
208 ATEASREAAAFAGDGSVYVERAVINPOHIEVQILGDRTEGEVHLYERDCSLQRHOKVVE 267
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
212 FRASYEAAQAFAGDGSILFVEKFERPHHIEVQLGDRHGNVHLYERDCSVQRHOKVVE 271
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
268 IAPAHLDPLDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFIEPNRIQVHEHTVT 327
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
272 IAPAPALPEGVREKILADALRLARHVGYQAGTVEFLVDQNGYFIEVNARLOVEHTVT 331
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
328 EETVEDLVKQMLAAGATLKLGLTQDKIKTHGAALOCRTTDPNNGFRPDTGTITA 387
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
332 EETIGVDLVQAQIRIAEGSLDLKLSQETIQTGSAIQCVTTEDPAKGFQDPSGRIV 391
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
388 YRSPGGAGVRLDGAALQGE-ITAFHDSMLVMTKCRGDFEFAVARAQAALAEFTVSGVA 446
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
392 FRSGEGMGLDASAFASVISPHYDSLMKVVIASARNHPNAAAKIRALKKIRGVK 451
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
447 TNGFRLALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLDVTVNKP- 502
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
452 TNPFLNLVLRQPSFLDASVDTYFIDEHPLEQFKPSQNAQKLLNLYGEVKNVGTPL 511
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
503 -HGVREPKDVAAPIDKLPNIKOLPLPGSRDRLKQLGPAFAFDLRQDALAVTDTFRDA 561
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
512 ATDLKPAVVPPIPIYIP--AGAKPPTGLRDLVLRQGTETFEKVEVSRPGCMITDTFRDA 569
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
562 HQSLLATRVRSFALKPAEAAVAKLTPPELLSVEAWGATYDVAMRFLFEDPWRDLRELA 621
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
570 HQSLLATRVRTYDMAAISPFVAQSFNGFLSLENGGATFEDVSMRFLHCPWELQTLRLK 629
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
622 MNVNITQMLRGENTVGYTPYDPSVCRVAFVKEAASGVDFIRFDALNDVDSQMRPAIDAV 681
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
630 IPNIPFQCLLRGANAMGYSYDNVYIKFCELAVKNGMDVFRVDSLNTLPNLLVGEAV 689
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
682 LETNTAVAEVAMAYSGDLSDPNEKLYTLDYILKMAEIVKSGAHILAIKDMAGLLRPAAV 741
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
690 GRAG-GVVEAAIAYTGDTYDKSKDYLDLKYIINLADQLVKAQAHLISIKDMAGVLKPEAA 748
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
742 TKLVTALRREF-DLPVHVHTHTAGQLATYFAAAQAGADAVDASAPISGTTSPSLSA 800
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
749 KLLIGALRKFDPIDPLHVHTHTDSAGVAAMLECAKAGADVDAVDAVDSMGTSQPSMGA 808
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
801 IVAAFATHTREDTGLSLEAVSDLEPYEAVRGLYLPFESGTGPTGR--VYRHEIPGGQLS 858
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
809 IVASLQGTAKHTGLSLDDISKYSAYWESTRQDYAPPECAITMKSGNADYVYKHEIPGGYT 868
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
859 NLRAQATLGLADREFELIBDNYAAVNEMLGRPTKTPPSKVYVGDALHLVAG- 912
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
869 NLQFAFSLGLQPGQDEVKRMVREANLVLDGLIKVTPSKIVGDLAQFVQNNLRITLV 928
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
913 DPADFAADPKYDIPDSVIAFLRGLGNPPGQWPEPLRTRALEGRS--EGKAPLTFVPEE 970
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
929 DRAD-----DLSPFKSVDFMQGNVGPYPYGFPEPLRTKVLRGKPKVDGR-----PGE 976
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
971 EQAHLDDADSK-----ERNSLNRLLPKPTTEFLHRRFRFGNTSLDRREFY 1019
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
977 NAKPVOLDAAKVELEEKHGTILSEEDVMSYSMFPTVFEDEFTRQOYGVVDKLPTRLELT 1036
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
1020 GLVEGRETLIRLPDYVRTPLVLRDLAISPPDDKGMNVVANVNGQIRPMVRDRSVESVTA 1079
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
1037 GLEIAEEVDVEIESGKT-LAIQLLAEGKLKNGEREVEFDLNGQMSIFVVDKASKELV 1095
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
1080 TAEKADSSNKGHVAAPFAG-VVTVVVAEGDEVKAGDAVAIEMKKEATITASVDGKIER 1138
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
1096 TRPRALPGVRGHIGAMPFGDVLLELKIKEGDKVTKKQPLFVLSAMKMWIDSPAGTVKA 1155
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
1139 VVVPAATKVEGDDLIVV 1156
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
1156 IHAPOGTKCSAGDLVVEV 1173
QY ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

RESULT 15

QYBYP

pyruvate carboxylase (EC 6.4.1.1) 1 [validated] - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein G3428; protein YGL062w; pyruvic carboxylase
C:Species: Saccharomyces cerevisiae
C:Date: 31-Dec-1991 #sequence_revision 19-Jul-1996 #text_change 01-Feb-2002
C:Accession: S64066; A29233; S05762; A29722
R:Feuermann, M.; Potier, S.; Souciet, J.L.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64044
A:Accession: S64066
A:Molecule type: DNA
A:Residues: 1-1178 <FEU>
A:Cross-references: EMBL:Z72584; NID:g1322565; PIDN:CAA96765.1; PID:g1322566; GSPDB:G
A:Experimental source: strain S288C
R:Lim, F.; Morris, C.P.; Ochojodor, F.; Wallace, J.C.
J. Biol. Chem. 263, 11493-11497, 1988
A:Title: Sequence and domain structure of yeast pyruvate carboxylase.
A:Reference number: A92662; MUID:88298805; PMID:3042770
A:Accession: A29233
A:Molecule type: DNA
A:Residues: 1-461 'G', 463-492 'D', 494-594 'A', 596-618 'Q', 620-663 'S', 665-771 'R', 773
A:Cross-references: EMBL:J03889; NID:g172101; PIDN:AAA34843.1; PID:g172102
R:Morris, C.P.; Lim, F.; Wallace, J.C.
Biochem. Biophys. Res. Commun. 145, 390-396, 1987
A:Title: Yeast pyruvate carboxylase: gene isolation.
A:Reference number: S05760; MUID:87241529; PMID:3036126
A:Accession: S05760
A:Molecule type: DNA
A:Residues: 1003-1178 <MOR>
A:Cross-references: EMBL:J03889
A:Accession: A29722
A:Molecule type: protein
A:Residues: 1124-1149 <MOR2>
C:Genetics:
A:Gene: SGD:PYC1; PYV; MIPS:YGL062w
A:Cross-references: SGD:S0003030; MIPS:YGL062w
A:Map position: 7L
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
C:Keywords: biotin binding; gluconeogenesis; homotetramer; ligase; zinc
F:21-478/Domain: biotin carboxylase homology <BCH>
F:157-331/Domain: ATP/bicarbonate binding #status predicted <ATB1>
F:353-468/Domain: ATP/bicarbonate binding #status predicted <ATB2>
F:569-908/Domain: ATP/bicarbonate binding #status predicted <PYR>
F:1096-1169/Domain: lipoyl/biotin-binding homology <LPB>
F:1135/Binding site: biotin (lys) (covalent) #status experimental
Query Match 41.9%; Score 2457; DB 1; Length 1178;
Best Local Similarity 46.6%; Pred. No. 3.6e-127; Mismatches 400; Indels 44; Gaps 16;
Matches 540; Conservative 175;
QY 31 KILVANRGEIAYRAFAALETGAATVAYIYPREDRGSFHRSEAVRIGTEG--SPVKAY 88
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
21 KILVANRGEIPIRIFRTAHELMSQVAVIYSHEDRLSTHKQKADAAVIVGEVQYTPVGAY 80
QY 89 LDIDEILGAKKVADATPYGVLSENAQALARECAENGITPTGTPDEVLDLTGDKSRAY 148
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
81 LAIDIEIISIAQKHQVDFTHPGYGFLSENSEFADKVVKAGITWIGPFAEVIDSVGDKVSAR 140
QY 149 TAAKAGLPLVAEST-PSKNIDDIVKSAEGQTYPIFVAVAGGGGMRFFVSPDELRLK 207
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
141 NLAAKANRVTVPCTPGPIETVEALDFVNEYGYPIIIRAAFGGGGGRVVRREGDDVADA 200
QY 208 ATEASREAAAFAGDGSVYVERAVINPOHIEVQILGDRTEGEVHLYERDCSLQRHOKVVE 267
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
201 FORATSEARTAGTNGTCFVERFLDKPKHIEVQLLADNHNHGVHLLFERDCSVQRHOKVVE 260
QY 268 IAPAHLDPELRDRIACADAVKFCRSIGYQAGTVEFLVDEKGNHVFIEPNRIQVHEHTVT 327
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
261 VAPAKTLPREVRDAIITDAVKLAKCEGYRNAGTAETFLVDNQNRHVFIEPNRIQVHEHTIT 320
QY 328 EETVEDLVKQMLAAGATLKLGLTQDKIKTHGAALOCRTTDPNNGFRPDTGTITA 387
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

Db 321 EETGIDIVAAQIQIAAGASLPOLGLFQDKITTRGFAIQCRITTEPAKNFQDPTGRIEV 380
QY 388 YRSPGGAGVRLDGA-QOLGGEITAHFDSMLVKMTCRGSDPETAVARAQALAEFTYSGVA 446
Db 381 YRSAGNGVRLDGNAYAGTII SPHYDSMLVKCSCSTYEVVRRKMIRALIEFRIRGVK 440
QY 447 TNGIFLRAILLREDEFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYLDVTVN----KP 502
Db 441 TNIPFLLTLTNVFTTEGYWTTTIDTTFOLFQFVSSQNRQAOKLLHLADVAVNGSSIKG 500
QY 503 HGVRPKDVAAPIDKLPNIKDL-----PLPRGSRDRKLGPAFAFARDLREODALA 552
Db 501 QICLPKXKSNP--SVPHLDAQGNVNVTKSAPPSGWRQVLLLEKGAFAFARQVRQNGTL 558
QY 553 VDTTTFRDAHQSLLATRVRSFALKPAAEAVALKTPELLSVEAWGATYDVAMRFLEFDPW 612
Db 559 LMDTTWRDAHQSLLATRVTHDLATTAPTAHALAGRALECEWGGATFDVAMRFLHEDPW 618
QY 613 DRDELREAMPNVNIOMLLGRNTVGYTPYDPSVCRAFVKEARASSGVDFIRFDALNDVS 672
Db 619 ERLKRLSVLPNPFOMLLRGANGVAYSSLPDNIADHFVQAKDNGVDIFRVFDALNDLE 678
QY 673 QMRPAIDAVLEINTAVAEAMAYSGDSDPENKLYTLDYLLKMAEEIVKSGAHILAKDM 732
Db 679 QLKVGVDVKKAG-GVVEATVCFSGDMLQPKK-YNLDIYLEIAEKIVQMGTHILGKDM 736
QY 733 AGLLRPAAVTKLVALRREF-DLPVHVHHDHAGQOLATYFAAAQAGADADGASAPLSG 791
Db 737 AGTKPAAAKLLIGSLRAKYDPDLP IHVTHDSAGTAVASMTACALAGADVVDVAINMSG 796
QY 792 TTSQPSLSAIVAAFAHTRDTGLSLEAVSDLEPYEAVRGLYLPESGTPGPTGRVYRHE 851
Db 797 LHSQPSINALLASL-BGNDTGTINVEHVRELDAYAEMLLYSCFEADLKGPDPVEYQHE 855
QY 852 IPGGQSLNRAQATALGLADREFELIEDNYAANEMLRPTKVTPSSKVVGDLALHLVGAG 911
Db 856 IPGGQTLNLLFQAQQLGLGEQWAEKRAYREANYLLGDIVKVTPTSKVVGDLAQPMVSNK 915
QY 912 VDPADFAADPOKYDIPDSVIAFLRGLGNPPGPGWPEPLTRALEGRSEKAPLTEYPEEE 971
Db 916 LTSDDVRLANSLDPFDSYMDFFEGILGQPYGGFEPFERSDVLNKK--RRKLTGRPGLE 972
QY 972 QAHLDAADSKEKRRNSLNL-----LFPKPTEEFLEHRRRFGNTSALDDREFFY 1019
Db 973 LEFFDLE--KIREDLQNRFGDVDECDVASNMPRVYEDFQKRETYGDLVLPTRSFLS 1030
QY 1020 GLVEGRETLIRLPDVRTLPLVRLDAISEPDDK-GMRNVVANYNGQIRPMRVDRSRVESVT 1078
Db 1031 PLETDEEIEVLEQGT-LIILQAVGDLNKKTGEREVYFDLNGEMRKIRVADRQKQVET 1089
QY 1079 ATAEXADSNKCHVAAPFAGV-VTVVAGDEVKAGDAVAITEAMKMEATITASVDGKTE 1137
Db 1090 VTKSKADMHDPLHIGAPMAGVIVEYVKHGSLLIKKQGPVAVLSAMKMEMIISPSDGOVK 1149
QY 1138 RVVVPAAATKVEGGDLIVV 1156
Db 1150 EVFVSDGENVDSDDLIVLL 1168

Search completed: September 24, 2003, 16:00:27
Job time : 40.259 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 15:44:03 ; Search time 18.6369 Seconds
(without alignments)
2919.469 Million cell updates/sec

Title: US-09-974-973A-2

Perfect score: 5865

Sequence: 1 MTAITLGLLLKGIITLST.....RVVPAATKVEGDLIVVVS 1157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2550.5	43.5	1178	1 PYC_MOUSE	Q05920 mus musculus
2	2534.5	43.2	1178	1 PYC_RAT	P52873 rattus norv
3	2531.5	43.2	1178	1 PYC_HUMAN	P11498 homo sapien
4	2457	41.9	1178	1 PYC1_YEAST	P11154 saccharomyc
5	2436	41.5	1180	1 PYC2_YEAST	P32327 saccharomyc
6	2393	40.8	1189	1 PYC_PICPA	P78992 pichia past
7	1079	18.4	501	1 PYCA_METJA	Q58626 methanococc
8	1032.5	17.6	447	1 ACCC_ANASP	Q06862 anabaena sp
9	1020	17.4	506	1 PYCA_ARCFU	O30019 archaeoglob
10	996	17.0	491	1 PYCA_METTH	O27939 methanobact
11	950	16.2	448	1 ACCC_HAEIN	P43873 haemophilus
12	940	16.0	449	1 ACCC_ECOLI	P24182 escherichia
13	938	16.0	449	1 ACCC_ECO57	Q8x9b6 escherichia
14	921	15.7	449	1 ACCC_PSEAE	P37798 pseudomonas
15	897	15.3	725	1 MCCA_HUMAN	Q96xq3 homo sapien
16	894	15.2	717	1 MCCA_MOUSE	Q99mr8 mus musculus
17	891.5	15.2	654	1 BCCA_MYCTU	P46401 mycobacteri
18	875	14.9	448	1 ACCC_BACSU	P49787 bacillus su
19	874.5	14.9	567	1 PYCB_METJA	Q58628 methanococc
20	869.5	14.8	598	1 BCCA_MYCLE	P46392 mycobacteri
21	869	14.8	703	1 PCCA_HUMAN	P05165 homo sapien
22	865	14.7	731	1 MCCA_SOYBN	Q42777 glycine max
23	862	14.7	734	1 MCCA_ARATH	Q42523 arabidopsis
24	842.5	14.4	704	1 PCCA_RAT	P14882 rattus norv
25	837.5	14.3	1835	1 DUR1_YEAST	P32528 saccharomyc
26	828	14.1	568	1 PYCB_METTH	O27179 methanobact
27	806	13.7	590	1 DCOA_SALTY	Q03030 salmonella
28	801.5	13.7	595	1 DCOA_KLEPN	P13187 klebsiella
29	620.5	10.6	2345	1 COAL_RAT	P11497 rattus norv
30	617.5	10.5	2324	1 COAC_CHICK	P11029 gallus gall
31	617.5	10.5	2346	1 COAL_HUMAN	Q13085 homo sapien
32	616.5	10.5	2346	1 COAL_BOVIN	Q9tts3 bos taurus
33	607.5	10.4	2346	1 COAL_SHEEP	Q28559 ovis aries

ALIGNMENTS

RESULT 1

ID	PYC_MOUSE	STANDARD;	PRT;	1178 AA.
AC	Q05920;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DE	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic			
DE	carboxylase) (PCB).			
GN	PC OR PCX			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Adipocyte;			
RC	MEDLINE=93189578; PubMed=8446588;			
RX	Zhang J., Xia W.L., Brew K., Ahmad F.;			
RA	"Adipose pyruvate carboxylase: amino acid sequence and domain			
RT	structure deduced from cDNA sequencing."			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:1766-1770(1993).			
CC	-!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,			
CC	INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY			
CC	ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE			
CC	CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE			
CC	SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY)			
CC	AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.			
CC	-!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) -> ADP + phosphate +			
CC	oxaloacetate.			
CC	-!- COFACTOR: BIOTIN AND MANGANESE.			
CC	-!- PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS.			
CC	-!- SUBUNIT: Homotetramer.			
CC	-!- SUBCELLULAR LOCATION: Mitochondrial matrix.			
CC	-!- TISSUE SPECIFICITY: LIVER, KIDNEY, ADIPOSE TISSUE, LIVER			
CC	AND BRAIN.			
CC	-!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES			
CC	AND CARBAMYL PHOSPHATE SYNTHETASES.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; L09192; AAA39737.1; -			
DR	PIR; A47255; A47255.			
DR	HSSP; P24182; LBNC.			
DR	SWISS-2DPAGE; Q05920; MOUSE.			
DR	MGD; MGI:97520; PCX.			
DR	InterPro; IPR001882; Biotin_attach.			
DR	InterPro; IPR005482; Biotin_carb_C.			
DR	InterPro; IPR000089; Biotin_lipoyl.			
DR	InterPro; IPR005479; CPase_L_D2.			

P32874 saccharomyc
Q00763 homo sapien
Q00955 saccharomyc
P78820 schizosacch
Q28994 archaeoglob
Q27077 methanobact
Q8dem2 vibrio vuln
Q8xa38 escherichia
Q9wz27 thermotoga
P00968 escherichia
P14846 salmonella

34 570.5 9.7 2273 1 HPA1_YEAST
35 560.5 9.6 2483 1 COA2_HUMAN
36 547.5 9.3 2233 1 COAC_YEAST
37 519 8.8 2280 1 COAC_SCHPO
38 267.5 4.6 1076 1 CARB_ARCFU
39 266 4.5 1060 1 CARB_METTH
40 255.5 4.4 1077 1 CARB_VIBVU
41 255 4.3 1072 1 CARB_ECO57
42 254.5 4.3 1099 1 CARB_THEMA
43 252.5 4.3 1077 1 CARB_VIBPA
44 252 4.3 1072 1 CARB_ECOLI
45 248.5 4.2 1074 1 CARB_SALTY

QY	651	VKEAASSGVDIRFDALNDVSRPAPDAVLETNTVAEVAMAYSGDLSDPNEKLTLD	710
Db	663	CEVAKENGMDYFRVFDLSUNYLPNMLGMEAAAGSAG-GWVEAAISYTGVDADPSRTKYSLE	721
QY	711	YLLKMAEIEIVKSGAHILAIKDMAGLLRPAAVTKLVLTALRREF-DLPVHVHTHTAGGOLA	769
Db	722	YYMGLAEELVRACTHILICIKDMAGLLKPACTMLVSSLRDFPDPLHIHTHTDSGAGVA	781
QY	770	TYFAAQAGADAVDAGASAPLSGTTSQPSLSAIVAFAAHRDRDTGLSLEAVSDLEPYWEAV	829
Db	782	AMLACAQAGADVVDVAVDMSMGMTSQPSMGALVACTKGTPLDTEVPLERVDYSEYWEGA	841
QY	830	RGVLVPFESGTPGPTGR--VYRHIEIPGGQSLNLRQAQATALGLADREFELIEDNTAAVNEML	887
Db	842	RGLTAAFDCTATMKSNGSDVTEYENIPGGQYTNLGHFQAHSMGLGSKFKEVKAYVEANQML	901
QY	888	GRPTKVTPTSSXVVGDLHLHVAGVDPADFAADPKQYDIPDSYIAFIRUGELGNPPGGWPE	947
Db	902	GDLLKVTPTSSKIVGDLAQFVQVNGLSRAEFAQAEELSFPRSVEFLOGYIGVPHGGFPE	961
QY	948	PLRTRAL-----EGRSEGKAPLITEVDEEQAHLDA-DDSKERNRNSLNRLFFPKPTEFL	1000
Db	962	PFRSKVLKDLFRIEGRFCASLPLNLNLEKDKLIDRHGEVTPEDVLSAAMYPDVTAQFK	1021
QY	1001	EHRRFNGTNSALDDREFFYGLIVEGRETLIRLPDVRTLLVRLDAISEPDDKGMRTVANV	1060
Db	1022	DFTATFGPLSLNTRLFLQGPKTAAEEFEVELERGKT-LHIALAVSDLNRAGQRQVFEL	1080
QY	1061	QOIRPMRVDRDRSVESYATAEAKDSNKGHVAAFPAG-VYTVTVAEGDEVKAGDAVATII	1119
Db	1081	NGQLRSILVKDTQAMKEMHFPKALKDVQSIGAPMPGKVIDIKVAAGDKVAKGQPLCVL	1140
QY	1120	EAMKWEATIASVDGKTIERVVPAATKVEGGDLIVV	1156
Db	1141	SAMKMETVTSPPXEGTIRKVHVTKDMTLEGGDLILEI	1177

RESULT 2

ID	PYC_RAT	STANDARD;	PRT;	1178 AA.
AC	P52873;	Q64555;		
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic			
DE	carboxylase) (PCB).			
GN	PC.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
EN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=96096548; PubMed=8522203;			
RA	Lehn D.A., Moran S.M., Macdonald M.J.			
RT	"The sequence of the rat pyruvate carboxylase-encoding cdna.";			
RL	Gene 165:331-332(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Wistar; TISSUE=Liver;			
RX	MEDLINE=96257760; PubMed=8687410;			
RA	Jitrapakdee S., Booker G.W., Cassidy A.I., Wallace J.C.;			
RT	"Cloning, sequencing and expression of rat liver pyruvate			
RT	carboxylase.";			
RL	Biochem. J. 316:631-637(1996).			
CC	-1- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,			
CC	INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY			
CC	ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE			
CC	CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE			
CC	SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY)			
CC	AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.			
CC	-1- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +			

```
CC CC
CC -1- COFACTOR: BIOTIN AND MANGANESE (BY SIMILARITY).
CC -1- PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS.
CC -1- SUBUNIT: Homotetramer (By similarity)
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC -----
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CC send an email to license@isb-sib.ch).
CC -----
CC EMBL; U32314; AAA96256.1; -
CC EMBL; U36585; AAC52668.1; -
CC PIR; S68252; JC4391.
CC HSP; P24182; IBNC.
CC DR DR
CC InterPro; IPR001882; Biotin_attach.
CC InterPro; IPR005482; Biotin_carb_C.
CC InterPro; IPR000089; Biotin_lipoyl.
CC InterPro; IPR005479; CPase_L_D2.
CC InterPro; IPR005481; CPase_L_N.
CC InterPro; IPR000891; HMGL-like.
CC InterPro; IPR003379; PYC_OADA.
CC InterPro; IPR005930; Pyruv_carbox.
CC Pfam; PF02785; Biotin_carb_C_1.
CC Pfam; PF00364; biotin_lipoyl_1.
CC Pfam; PF00289; CPase_L_chain_1.
CC Pfam; PF02786; CPase_L_D2_1.
CC Pfam; PF00682; HMGL-like; 1.
CC Pfam; PF02436; PYC_OADA; 1.
CC TIGRPFAMS; TIGR01235; pyruv_carbox; 1.
CC PROSITE; PS00188; BIOTIN; 1.
CC KW Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;
CC ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide.
CC FT TRANSIT 1 20
CC FT CHAIN 21 1178
CC FT DOMAIN 21 549
CC FT DOMAIN 550 1000
CC FT DOMAIN 1096 1178
CC FT NP_BIND 198 203
CC FT ACT_SITE 328 328
CC FT BINDING 1144 1144
CC FT CONFLICT 222 222
CC FT CONFLICT 866 866
CC FT CONFLICT 977 977
CC FT SEQUENCE 1178 AA; 129689 MW; 8E5FA19BC132A8DD CRC64;
CC Query Match 43.2%; Score 2534.5; DB 1; Length 1178;
CC Best Local Similarity 46.2%; Pred. No. 6.3e-126;
CC Matches 544; Conservative 188; Mismatches 409; Indels 37; Gaps 14;
QY 7 GGLLKGIITLVSTHTSSTLPA-----FKKILVANRGELAVRAAFRAALETGAA 54
Db 9 GGRLLGV-----RRSSTAPVASPNVRLEYKPKIKVMVANRGELAIIVRFACIELGIR 62
QY 55 TVAIYPREDGRGFHSFASAEAVRIGTEGSPVKAYLDIDIEIGAANKVDADIPYGVFUS 114
Db 63 TVIYSEQDTGMQHROKADAEYALIGRLAPVGQYLIHPDIIKVAKENGVDVAHPGVGFUS 122
QY 115 ENAQLARECAENGITFIGPTPEVLDTGDKSAVTAAKKAGLPVL-AESTPSKNIDDIIVK 173
Db 123 ERADFQAQCQDAGVRFGISPEVVRKMGMKDVKEARATAAGVVVPVPGTINSPLREAHF 182
QY 174 SAEGQTPIPVKAVAGGGGGRGMRFPSSPDLEKLATASREAEAAGDGSVVVERAVINP 233
Db 183 FSNYTGFPFIIFKAAVGGGGRGMRVHVSYEELNENTRAYPEALAFNGCALVEKFEIKP 242
QY 234 QHIEVOILDRTGEVHVHYERDCSLQRHQKVVEIAPAHLDELPELRDICADVAFCRSI 293
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GN PC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN PC SEQUENCE FROM N.A.
 RP TISSUE=Kidney, and Liver;
 RC MEDLINE=95002202; PubMed=7918683;
 RA Wexler I.D., Du Y., Lisgaris M.V., Mandal S.K., Freytag S.O.,
 RA Yang B.-S., Liu T.-C., Kwon M., Patel M.S., Kerr D.S.;
 RT "Primary amino acid sequence and structure of human pyruvate
 RT carboxylase.";
 RL Biochim. Biophys. Acta 1227:46-52(1994).
 RN [2]
 RN PC SEQUENCE FROM N.A.
 RP TISSUE=Kidney;
 RC MEDLINE=94324922; PubMed=8048912;
 RA Mackay N., Rigat B., Douglas C., Chen H.S., Robinson B.H.;
 RT "cDNA cloning of human kidney pyruvate carboxylase.";
 RL Biochem. Biophys. Res. Commun. 202:1009-1014(1994).
 RN [3]
 RN PC SEQUENCE FROM N.A.
 RP TISSUE=Kidney, and Liver;
 RC Walker M.E., Jitrapakdee S., Val D.L., Wallace J.C.;
 RA Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RN PC SEQUENCE FROM N.A.
 RP TISSUE=Lung;
 RC MEDLINE=23388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udsit T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RN PC SEQUENCE OF 1083-1178 FROM N.A.
 RP MEDLINE=87212051; PubMed=3555348;
 RA Lamtonwan A.-M., Quan F., Gravel R.A.;
 RT "Sequence homology around the biotin-binding site of human propionyl-
 RT CoA carboxylase and pyruvate carboxylase.";
 RL Arch. Biochem. Biophys. 254:631-636(1987).
 RN [6]
 RN PC SEQUENCE OF 1135-1178 FROM N.A.
 RP MEDLINE=85030380; PubMed=6548474;
 RA Freytag S.O., Collier K.J.;
 RT "Molecular cloning of a cDNA for human pyruvate carboxylase.
 RT Structural relationship to other biotin-containing carboxylases and
 RT regulation of mRNA content in differentiating preadipocytes.";
 RL J. Biol. Chem. 259:12831-12837(1984).
 RN [7]
 RN PC VARIANTS PC DEFICIENCY THR-610 AND ILE-743.
 RP MEDLINE=98254451; PubMed=9585612;
 RA Carbone M.A., MacKay N., Ling M., Cole D.E.C., Douglas C., Rigat B.,
 RA Reigenbaum A., Clarke J.T.R., Haworth J.C., Greenberg C.R.,
 RA Seargeant L., Robinson B.H.;
 RT "American pyruvate carboxylase deficiency is associated with two
 RT distinct missense mutations.";

Am. J. Hum. Genet. 62:1312-1319(1998).
 [8]
 RN PC VARIANTS PC DEFICIENCY ALA-145 AND CYS-451.
 RP MEDLINE=98244401; PubMed=9585002;
 RA Wexler I.D., Kerr D.S., Du Y., Kaung M.M., Stephenson W., Lusk M.M.,
 RA Wappner R.S., Higgins J.J.;
 RT "Molecular characterization of pyruvate carboxylase deficiency in two
 RT consanguineous families.";
 RL Pediatr. Res. 43:579-584(1998).
 RN CC -!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
 CC INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
 CC ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE
 CC CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE
 CC SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY)
 CC AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.
 CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO₃(-)- = ADP + phosphate +
 CC oxaloacetate.
 CC -!- COFACTOR: BIOTIN AND MANGANESE.
 CC -!- PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -!- DISEASE: Defects in PC are the cause of pyruvate carboxylase
 CC deficiency (PC deficiency) [MIM:266150] leading to lactic
 CC acidosis, mental retardation and death. It occurs in three forms:
 CC mild or type A, severe neonatal or type B, and a very mild
 CC lacticacidemia.
 CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
 CC AND CARBAMYL PHOSPHATE SYNTHETASES.
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 CC -----
 DR EMBL: U04641; AAA99537.1; -;
 DR EMBL: S72370; AAB31500.1; -;
 DR EMBL: UC0891; AAA82937.1; -;
 DR EMBL: BC011617; AAH11617.1; -;
 DR EMBL: M26122; AAA36423.1; -;
 DR EMBL: K02282; AAA60033.1; -;
 DR F1R; G01933; JC2460.
 DR HSSP; P24182; IBNC.
 DR Genew; HGNC:8636; PC.
 DR GK; P11498; -;
 DR MIM; 266150; -;
 DR GO; GO:0005524; F:ATP binding activity; TAS.
 DR GO; GO:0003374; F:biotin binding activity; TAS.
 DR GO; GO:0004736; F:pyruvate carboxylase activity; TAS.
 DR InterPro; IPR001882; Biotin_attach.
 DR InterPro; IPR005482; Biotin_carb_C.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR InterPro; IPR005479; CPase_L_D2.
 DR InterPro; IPR005481; CPase_L_N.
 DR InterPro; IPR000891; HMGL-like.
 DR InterPro; IPR003379; PYC_OADA.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF00364; biotin_lipoyl; 1.
 DR Pfam; PF00289; CPase_L_chain; 1.
 DR Pfam; PF02786; CPase_L_D2; 1.
 DR Pfam; PF00682; HMGL-like; 1.
 DR Pfam; PF02436; PYC_OADA; 1.
 DR TIGRFAMS; TIGR01235; PYRUV_carbox; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 KW Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;
 KW ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide;
 KW Disease mutation.
 FT TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
 FT CHAIN 21 1178 PYRUVATE CARBOXYLASE.
 FT DOMAIN 21 549 BIOTIN CARBOXYLASE (BY SIMILARITY).

DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pyruvate carboxylase 2 (EC 6.4.1.1) (Pyruvic carboxylase 2) (PCB 2).
 GN PYC2 OR YBR218C OR YBR1507.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=92017667; PubMed=1921979;
 RX Stucka R., Deguin S., Salmon J.-M., Gancedo C.;
 RT "DNA sequences in chromosomes II and VII code for pyruvate
 carboxylase isoenzymes in Saccharomyces cerevisiae: analysis of
 pyruvate carboxylase-deficient strains."; Mol. Gen. Genet. 229:307-315(1991).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=S288c;
 RA Dubois E., el Bakkoury M., Glansdorff N., Messenguy F., Pierard A.,
 RA Scherens B., Vierendeels F.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96128067; PubMed=8554526;
 RA Val D.L., Chapman-Smith A., Walker M.E., Cronan J.E. Jr.,
 RA Wallace J.C.;
 RT "Polymorphism of the yeast pyruvate carboxylase 2 gene and protein:
 effects on protein biotinylation."; Biochem. J. 312:817-825(1995).
 RL [4]
 CC -!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
 INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
 ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE
 CARBOXYL GROUP TO PYRUVATE IN THE SECOND.
 CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
 oxaloacetate.
 CC -!- COFACTOR: BIOTIN AND ZINC.
 CC -!- PATHWAY: Gluconeogenesis.
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- INDUCTION: By glucose.
 CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPONAMIDE TRANSFERASES
 AND CARBAMYL PHOSPHATE SYNTHETASES.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X59890; CAA42544.1; -
 DR EMBL; Z36087; CAA85182.1; -
 DR EMBL; U35647; AAC49147.1; -
 DR PIR; S46094; S46094.
 DR HSP; P24182; IBNC.
 DR SGD; S0000422; PYC2.
 DR GO; GO:0005829; C:cytosol; IDA.
 DR GO; GO:0004736; F:pyruvate carboxylase activity; IDA.
 DR InterPro; IPR001882; Biotin_attach.
 DR InterPro; IPR005482; Biotin_carb_C.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR InterPro; IPR005479; CPase_L_D2.
 DR InterPro; IPR005481; CPase_L_N.
 DR InterPro; IPR000891; HMGL-like.
 DR InterPro; IPR003379; PYC-OADA.
 DR InterPro; IPR005930; Pyruv_carbox.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF00364; biotin_lipoyl; 1.
 DR Pfam; PF00289; CPase_L_chain; 1.
 DR Pfam; PF02786; CPase_L_D2; 1.

DR Pfam; PF00682; HMGL-like; 1.
 DR Pfam; PF02436; PYC_OADA; 1.
 DR TIGRFAMS; TIGR01235; pyruv_carbox; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 DR PROSITE; PS00866; CPASE_1; 1.
 DR PROSITE; PS00867; CPASE_2; 1.
 KW Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
 KW Zinc; Multigene family.
 FT NP_BIND 183 188 ATP (POTENTIAL).
 FT ACT_SITE 313 313 BY SIMILARITY.
 FT BINDING 1136 1136 BIOTIN (BY SIMILARITY).
 FT CONFLICT 15 15 S -> C (IN REF. 1).
 FT CONFLICT 132 132 D -> E (IN REF. 1).
 FT CONFLICT 238 238 N -> K (IN REF. 1).
 FT CONFLICT 268 268 L -> F (IN REF. 1).
 FT CONFLICT 546 546 S -> C (IN REF. 1).
 FT CONFLICT 642 642 N -> T (IN REF. 1).
 FT CONFLICT 771 773 GTA -> STR (IN REF. 1).
 FT CONFLICT 831 831 W -> R (IN REF. 1).
 FT CONFLICT 839 839 S -> P (IN REF. 1).
 FT CONFLICT 1001 1001 Y -> N (IN REF. 1).
 FT CONFLICT 1155 1155 K -> R (IN REF. 1).
 FT CONFLICT 1178 1178 Q -> P (IN REF. 1).
 FT CONFLICT 1180 1180 K -> KVIFTR (IN REF. 1).
 SQ SEQUENCE 1180 AA; 130166 MW; AD60DA3A60F5E001 CRC64;
 Query Match 41.5%; Score 2436; DB 1; Length 1180;
 Best Local Similarity 45.5%; Pred. No. 9.6e-121;
 Matches 530; Conservative 185; Mismatches 407; Indels 44; Gaps 16;
 QY 24 SLPAPFKILVANRGEIAVRAFAALETGAATVAIYPREDRGSFHSFSAEAVRIGTEG- 82
 DB 15 SLLGKKNKLLVANRGEIPTRIFRSAHLSMRTIATYSHEDRLSMHRLKADAEAVIGEEQ 74
 QY 83 -SPVXAYLDIDELIGNAKKVKADAIYPGYGFLSENQALRECAENGITFIGTPEVLDLT 141
 DB 75 YTPVGAYTAMDEIIEITAKKHVDFTHPGYGFUSEFADKVVYKAGITWGGPAEVIDSV 134
 QY 142 GDKRAVTAACKAGLPVLAEST-PSKNIDDIKVSABGQYPIFVKAVAGGGRGMFVS 200
 DB 135 GDKVSARHLAARANVTPVETPGTPIETVQEAALDFVNEYGYPIIKAFFGGGGRMVRVE 194
 QY 201 PELKRLATEAREAEAFAGDGSVYVERAVINPQHIEVQILGDRGTGEVHLVDERCSLOR 260
 DB 195 GDVDADAFORATSEARTAFNGTCFVERFLDKPKHIEVQLLADNHNHGVVHLFERDCSVOR 254
 QY 261 RHQVVEIAPAOHLPELDRDICAADAKFCRSIGOGAGTVEFLVDEKGNHVFIEKNPRI 320
 DB 255 RHQVVEVAPAKTLPREVRDAILTDAVLAKVCGYRNAGTAFLVDNQNHRHFIENPRI 314
 QY 321 QVEHTVTEEVTVDLVKAQMLAAGATKELGLTQDKIKHGAALQCRITTEDPNNNGFRP 380
 DB 315 QVEHTITEITGIDIVSAQIQIAAAGATLTQLGLQDKITTRGFSIQCRITTEDPSKNFQP 374
 QY 381 DTGTTATYSPGAGVRLDGA-AQLGGEITAFHDSMLVMTCRGSDFFETAVARAQALAE 439
 DB 375 DTGRLEVYSAGNGVRLDGGNAYAGATISPHYDSMLVKSCSGSTYETVRRKMLRALIE 434
 QY 440 FTVSGVAVNIGELRALRREDEFTSKRIATGFTGDHPHLQLQAPPADDEQGRDLYLADVIV 499
 DB 435 FAIRGVKINIPFLLLILLNPVEIGTYWTTFTDDTQPLQFQWVSSONRAQKLHLHYLADLAV 494
 QY 500 N-----KPHGVREKDVAAPIDKLPNIKDL-----PLPRGSRDLKQLGFAAFARDL 545
 DB 495 NGSSIKQIGLPLKLSNP--SVPHLDAQNVINVTKSAPPSSGWQVLEKGPSEFAKQV 552
 QY 546 REQDALAVTDITFRDAHOSLLATRVRSFALKPAAEAAVAKLIPELLISVWAGGATDVAMR 605
 DB 553 RQFNGLTLLMDITWRDAHOSLLATRVTHDLAPTAPTTAHALAGAFALCWCWGATDVAMR 612
 QY 606 FLFEDPWDRDLDELREAMPNVNIQMLLRGNTVGYTPYDSCVCRAPVKAASSGVDIRF 665
 DB 613 FLHEDPWDRDLDELREAMPNVNIQMLLRGNTVGYTPYDSCVCRAPVKAASSGVDIRF 672

QY 666 DALNDVQMRPAIDAVLENTAVAEVAMAYSGDLSDPNEKLYTLDYLLKMAEIVKSGAH 725
 D 673 DALNDLEQLKGVNAVKKAG-CVVEATVYCSGDMQLPGKK-YNLDYILEVEKIVQMGTG 730
 QY 726 ILAIDKMAGLRPAAVTKLVLTALREF-DLPVHVHTHTAGQLATYFAAQAQAGADAVG 784
 D 731 ILIGKDMAGTKPAAAKLLIGSLRTPDLPHTVHSHDSAGTAVASMTACALAGADVVDV 790
 QY 785 ASAPLSGTTSPSLSAIAFAHTRDRTGLSLEAVSDLEPYEAVRGVLYLPESCPTGPT 844
 D 791 AINSMGLTSQPSINALASL-EGNIDIGINVEHVRELDAYAEMLLYSCFADLKGPD 849
 QY 845 GRVYHEIPGGQLSNLQAATLALGADRFELIEDNYAAVNEMLGRTKVPSPSKVVGDLA 904
 D 850 PEVYQHEIPGGQLTNLLFQAQGLGGEQWAEKRAYREANVLLGDIVKVTPTSKVVGDLA 909
 QY 905 LHLVAGVDPADFAADPKYDIPDSVIAFLGELGNPPGGWPEPLRTALGERSGKAPL 964
 D 910 QPMVSNKTSDDIRKLANSLDFPDVMDFFELIGQPYGGFPEPLRSVLRNK---RRKL 966
 QY 965 TEVPEEQAHLDADDKERNLSNRL-----LFPKPTBEFLEHRRRRFGNTSAL 1012
 D 967 TCRGLELEPPLE--KIREDLQNRFGIDECDAVSYNRYPRVYEDFKIRETYGDLVL 1024
 QY 1013 DREFYGLVGEFRELILKLPVVRTPLLVRLDAISEPDDK-GMRNVYVANNVGOIRPMYRD 1071
 D 1025 PTKNPLAEPDEEIEVTEIOGKT-LIILQAVGLNKKTGQREYVYFELNGELKIRVAD 1083
 QY 1072 RSVESVATATBAKSSNGHVAAPFAGV-VTVVAEGDEVKAGDAVAIEAMKMEATITA 1130
 D 1084 KSONTSQVAKPAQADVDHTQIGAPMAGVLIIEVKHGLSVLKGESIAVLKAMNEMVSS 1143
 QY 1131 SVDGKIERVVPAAATKVEGGLIVV 1156
 D 1144 PADGOVKDFIKDGSVDASDLLVL 1169

RESULT 6

QY ID PYC_PICPA STANDARD; PRT; 1189 AA.
 AC P78992;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Pyruvate carboxylase (EC 6.4.1.1) (Pyruvic carboxylase) (PCB).
 GN PYC1.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxId=4922;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98301182; PubMed=9639311;
 RA Menendez J., Delgado J., Gancedo C.;
 RT "Isolation of the Pichia pastoris PYC1 gene encoding pyruvate
 RT carboxylase and identification of a suppressor of the pyc
 RT phenotype.";
 RL Yeast 14:647-654(1998).
 CC -!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
 CC INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
 CC ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE
 CC CARBOXYL GROUP TO PYRUVATE IN THE SECOND (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
 CC oxaloacetate.
 CC -!- COFACTOR: BIOTIN AND ZINC.
 CC -!- PATHWAY: Gluconeogenesis.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
 CC AND CARBAMYL PHOSPHATE SYNTHETASES.

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CC EMBL; Y11106; CAA71993.1; -.
 DR HSSP; P24182; 1DVI.
 DR InterPro; IPR001882; Biotin_attach.
 DR InterPro; IPR005482; Biotin_carb_C.
 DR InterPro; IPR000899; Biotin_lipoyl.
 DR InterPro; IPR005483; CPase_L.
 DR InterPro; IPR005479; CPase_L_D2.
 DR InterPro; IPR005481; CPase_L_N.
 DR InterPro; IPR000891; HMGL-like.
 DR InterPro; IPR003379; PYC_OADA.
 DR InterPro; IPR005930; Pyruv_carbox.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF00364; biotin_lipoyl; 1.
 DR Pfam; PF00289; CPase_L_chain; 1.
 DR Pfam; PF02786; CPase_L_D2; 1.
 DR Pfam; PF00682; HMGL-like; 1.
 DR Pfam; PF02436; PYC_OADA; 1.
 DR PRINTS; PR00098; CPASASE.
 DR TIGRFAMs; TIGR01235; pyruv_carbox; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 DR PROSITE; PS00866; CPASE_1; 1.
 DR PROSITE; PS00867; CPASE_2; 1.
 KW Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
 KW Zinc.
 FT NP_BIND 185 190 ATP (POTENTIAL).
 FT ACT_SITE 315 315 BY SIMILARITY.
 FT BINDING 1140 1140 BIOTIN (BY SIMILARITY).
 SQ SEQUENCE 1189 AA; 131400 MW; 8B6B58079657914 CRC64;

Query Match 40.8%; Score 2393; DB 1; Length 1189;
 Best Local Similarity 45.5%; Pred. No. 1.8e-118;
 Matches 529; Conservative 176; Mismatches 419; Indels 38; Gaps 18;
 QY 23 SSTLPAPKILVANRGEIAVRAALETGAATVAIYPREDRGSFHRFSASAVRIGTEG 82
 D 16 SLLGTMMKILVANRGEIPDIRFRTAHELSTMTVAIYSHEDRLSMRLKADAEYVIGERG 75
 QY 83 --SPVKAYLDIDEIIGAARKVKADAIYPGYFLSENAQLARECAENGITFTGPTPEVLDL 140
 D 76 QYSPVOAYLAIDEIITKIAVKHNVNMIHPGYFCSENSEFARKVEENGILWVGPSDTVIDA 135
 QY 141 TGDKSRAVTAAKKAGLPVLAESTPSKNTDDIVKS---AEGQTYPTFFKAVAGGGRGMR 197
 D 136 VGDKVSARNLAYAANVPTV-PGTPGP-IEDVAQATAFVEEYGPYVIAKAAFGGGGRMRV 193
 QY 198 VSSPDELKRLATEASREAAAFDGSVYVRAVINPOHIEVQIILGDRTGEVVHLYERDCS 257
 D 194 VREGDDIEDATLRASSEAKTAGNCTVFIEFLDKPHIEVQLADANVNIHLFERDCS 253
 QY 258 LQRHQKVVEIAPAOHLDELDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEMN 317
 D 254 VORRHQKVARNCSAKTLPEVVRNALNDVAKLAKTANYRNAGTAETFLVDSQNRHYFIEIN 313
 QY 318 PRIQVEHVTVTEVTEVDLVKQOMRLAAGATLKEGLTODKTKTHCAALOCRTTDDPNNG 377
 D 314 PRIQVEHITTEITGVDIVAAQIQIAGASLEQLGLEKITTTRGFATCQRTTDEDTKN 373
 QY 378 FRPDTGTTATYSGGAGVRLDGAALGGE-ITAFHDSMLVKMTCRGSDFETAVARAQRA 436
 D 374 FQPDGTGKLEVYSSGGNGVRLDGGNGFAGAVISHYDSMLVKCSTSGSNYIRKKMIRA 433
 QY 437 LAETVSGVAVNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEGRILDYAD 496
 D 434 LVEFRIRGVKTNIPFLALLTPHVFMTSECTWTTFIDTPELFKILTSQNAQKLLAYLGD 493
 QY 497 VTVN-----KPHGVPRKDVAAPIDKLPNIKD--LPLPRGSRDLKQLGPAFAAF 543

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494 LAVNGSSIKQIGLKLH--KEADIFSTIDNGVDVDSIPPPDQWQRFLEKGPQFAQ 551
QY 544 DLREQDALAVTQTRDASHOSLALTRVRSFALKPAEAVAKLTPELLSVEANGATYDVA 603
Db 552 QVRAPEGLMINTTWRDAHOSLALTRVTHDLINTAPATSYALHRAFALECGWGATFDVS 611
QY 604 MRLFEDEPDWDLDELREAMPNYNIOMLLGRNTVGYTPYDVCRAFYKAEAAASSGVDPFR 663
Db 612 MRLFEDEPDWDLDELREAMPNYNIPFMSMLLRGGNGVAYISLPDIAHFLKQAKDTGVDFR 671
QY 664 IFDALNDVSOMPADAVLETNTVAEVAAMAYSGDLSDPNEKLYLDLYLKMAEIVKSG 723
Db 672 VEDALINDEQLKGVGDVAKKAG-GVVEATPMCYSGDMLKPKKK-YNLEYVINLATEIVG 729
QY 724 AHILAIDKMGALRLPAATKLVTLARREF-DLPVHVHTHTAGGOLATYFAAAQAGADV 782
Db 730 THILAVKMGAGTLKTAQKQLISALRRKPPSLPIHVHTHDSAGTVASMVACARAGADV 789
QY 783 DGASAPLSGTTTQSPLSATAFAHTRDTGLSLEAVSDLEPYWEAVRGLYLFPFSGTPG 842
Db 790 TVRVNMSMGMTSOPSMSAFIASL-DGEITGTIPENAREIDAYWAEMLLYSCFEADLKG 848
QY 843 PTGRVYRHEIPGOLSNLRAQATFALGLADRFELIEDNTAAVNEMLRPTKVTPTSSKVGVD 902
Db 849 PDPEVTHQHEIPGGQTLNLLFQAQQGLGKWKVETKAYFAANRLLDGIIVKVTPTSKVGVD 908
QY 903 LALHLVAGVDPADFAADPPKQYDIPDSVIAFLRGLGNPPGWPPLRLTRALEGRSE--- 959
Db 909 LAQFVSNKLSSEDEVERLASELDFDPSVLDFEGLMGTFYGGFPPLRTNVISGRRKLT 968
QY 960 GKAPLITEVPEEQA---HLDADDKERNLSL-NRLLFPKPTPEEFLEHRRRFGNTSALDDR 1015
Db 969 SRPGLTLEPYNIPAIREDLEARFSKVTENDVASYNNPKVYKAYKKQBELYDGLSVLPTR 1028
QY 1016 EFYF--GLVEGRETLIRLPDVRTPLLVRLDAISE-PDOKGMNVVANYNGQIRPMRVEDR 1072
Db 1029 NFLSPKIDEERHVTIVITETKTLIIKCMAGELSSQSGTREVYFELNGEMRKVTVEDK 1088
QY 1073 SVESVATAKADSNKNGEVAAPFAGVVT-VTVAEQDEVKAGDAVAITEAKMEATITAS 1131
Db 1089 NGAVETITRPKADAHNPENIGAPMAGVVVEVVRHENGVEKKGDPITAVLSAKMEMVISP 1148
QY 1132 VDGKTERVVVPAATKVEGDLI 1153
Db 1149 VAGRTIGQIAVKNDSVDASDLI 1170

RESULT 7
PYCA_METJA
ID PYCA_METJA STANDARD; PRT: 501 AA.
AC Q58626;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic carboxylase A).
GN PYCA OR M1229.
OS Methanococcus jannaschii.
OC Archaea: Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=868087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Cocayne J.D.,
RA Kervlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.P., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT *Complete genome sequence of the methanogenic archaeon, Methanococcus

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RT jannaschii.";
RL Science 273:1058-1073(1996).
RN [2]
RP SEQUENCE OF 1-12, AND FUNCTION.
RX MEDLINE=21034791; PubMed=11195096;
RA Mukhopadhyay B., Patel V.J., Wolfe R.S.;
RT "A stable archaeal pyruvate carboxylase from the hyperthermophile
RT Methanococcus jannaschii.";
RL Arch. Microbiol. 174:406-414(2000).
CC -1- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
CC INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
CC ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL
CC GROUP TO PYRUVATE IN THE SECOND.
CC -1- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
CC oxaloacetate.
CC -1- COFACTOR: ATP, MAGNESIUM (OR MANGANESE OR COBALT), PYRUVATE AND
CC BICARBONATE.
CC -1- ENZYME REGULATION: INHIBITED BY MAGNESIUM, WHEN ITS CONCENTRATION
CC EXCEEDED THE ATP ONE, AND BY HIGH CONCENTRATION OF ATP AND ALPHA-
CC KETOGLUTARATE.
CC -1- PATHWAY: Gluconeogenesis.
CC -1- SUBUNIT: HETEROOCTAMER OF FOUR A AND FOUR B SUBUNITS.
CC -1- MASS SPECTROMETRY: MW=55500; METHOD=WALDI.
CC -1- MISCELLANEOUS: ITS OPTIMUM PH IS 8.5 AND THE OPTIMUM TEMPERATURE
CC IS 80-90 DEGREES CELSIUS.
CC -1- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC -----
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CC EMBL; U67563; AAB99232.1; -
CC PIR; D64453; D64453.
CC DR HSP; P24182; 1BNC.
CC DR TIGR; M1229; -
CC DR InterPro; IPR004549; AccC.
CC DR InterPro; IPR005482; Biotin_carb_C.
CC DR InterPro; IPR005483; CPase_L.
CC DR InterPro; IPR005479; CPase_L_D2.
CC DR InterPro; IPR005481; CPase_L_N.
CC DR Pfam; PF02785; Biotin_carb_C; 1.
CC DR Pfam; PF00289; CPase_L_chain; 1.
CC DR Pfam; PF02786; CPase_L_D2; 1.
CC DR PRINTS; PR00098; CPASE.
CC DR TIGRFAMs; TIGR00514; accC; 1.
CC DR PROSITE; PS00866; CPASE_1; 1.
CC DR PROSITE; PS00867; CPASE_2; 1.
CC DR Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
CC ATP-binding; Complete proteome.
CC NP_BIND 162 167 ATP (POTENTIAL).
CC ACT_SITE 291 291 POTENTIAL.
CC FT ACT_SITE 291
CC SQ SEQUENCE 501 AA; 55402 MW; 04D2E401892F872F CRC64;
Query Match 18.4%; Score 1079; DB 1; Length 501;
Best Local Similarity 48.0%; Pred. No. 8.5e-50;
Matches 217; Conservative 85; Mismatches 144; Indels 6; Gaps 4;
QY 29 FKKILVANRGEIAVRAFAALETGAATVAIYPRDRGSHFRSFASEAVRIGTEGSPVKAY 88
Db 2 ENKVLINRGETAIRIRACWELGKTVAVYSEADKRSUHLATLADAEVCIG-PAPAASKY 60
QY 89 LDIDEIIGAARKVADALPYGYGLFSENAQLARCAENGITFPGTPEVLDTGDKSRAY 148
Db 61 LNIIDAILNVAEKAKVDALHPGYGLFSENAQLARCAENGITFPGTPEVLDTGDKSRAY 120
QY 149 TAAKAGLPLVAESTPS-KNIDDIVKSAEGOTPIFYKAVAGGGGGRGMRFYSSPDELRL 207
Db 121 KIMKAGVPLIPGSEGAIEDIDEAIEIAETGFPVVVKASAGGGGGMVSAYSKEELKEY 180

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[illegible]

SQ SEQUENCE 447 AA; 49104 MW; 8A541B38B39E00F9 CRC64;

Query Match 17.6% Score 1032.5 DB 1: Len

QY 89 LDIDEIIGAAKVKKADAIYPGYGFLSENAQLARECAENGITFIQIP

QY 264 KVVETAPQAHLDPEDRDRICADAVKFCRSIGYQGAGTVEFLVDEK

Db 238 KLEEEAPSPALDSDLREKMGQAAVKAQFINYTGAGTIEFLDLS

324 HTVTEFVTEVDLYKAOMRLAAGATIKELGITODKIKTHCAALOCB

209 HRYTEMTCOVITVEOTPIACBBIB--ETADONUTBOUNTED

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52. ЗАКЛЮЧЕНИЕ	53
53. СПИСОК ЛИТЕРАТУРЫ	54
54. ПРИЛОЖЕНИЯ	55
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98. ПРИЛОЖЕНИЯ	99
99. ДОПОЛНИТЕЛЬНЫЕ МАТЕРИАЛЫ	100
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101. СПИСОК ЛИТЕРАТУРЫ	102
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103. ДОПОЛНИТЕЛЬНЫЕ МАТЕРИАЛЫ	104
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126. ПРИЛОЖЕНИЯ	127
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QY 304 ITAIKSPGGAGVKLDGGAQQLGGELIAHFDLSMLVAMTICKGSDFE

D6 355 RISGYLPGGGVRIDSHVYTDYQIPPPYDSLIGKLIWGPDRAI

QY 444 GVATNIGFLRALLREEDFTSKRIATGFI 471

Db 415 GLPTTIGFHQRMENPQFLQGNVSTSFV 442

RESULT 9
PYCA ARCFU

ID	PYCA_ARCFU	STANDARD;	PRT;	506 AA.
AC	Q30019.			

DT 30-MAY-2000 (Rel. 39, Created)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DT 30-MAY-2000 (Rel. 33, Last sequence update)

DE Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic c
GN PYCA OR AF0220.

OS Archaeoglobus fulgidus.

Archaeoglobaceae; Archaeoglobus.

OX NCBL_TaxID=2234;

CC AND CARBAMYL PHOSPHATE SYNTHETASES.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: A5000942; AAB86377.1; -
 CC DR PIR: A69123; A69123.
 CC DR HSP: P24182; IBNC.
 CC DR InterPro: IPR004549; AccC.
 CC DR InterPro: IPR005482; Biotin_carb_C.
 CC DR InterPro: IPR005479; CPhase_L_D2.
 CC DR InterPro: IPR005481; CPhase_L_N.
 CC DR Pfam: PF02785; Biotin_carb_C; 1.
 CC DR Pfam: PF02829; CPhase_L_D2; 1.
 CC DR Pfam: PF02786; CPhase_L_D2; 1.
 CC DR TIGRFAMs: TIGR00514; accC; 1.
 CC DR PROSITE: PS00866; CPSASE_1; 1.
 CC DR PROSITE: PS00867; CPSASE_2; 1.
 CC DR Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
 CC ATP-binding; Complete proteome.
 CC KW ATP-binding; Complete proteome.
 CC FT NP_BIND 162 167 POTENTIAL.
 CC FT ACT_SITE 291 291
 CC SQ SEQUENCE 491 AA; 54656 MW; 5789C34DA7475C2E CRC64;
 CC -----
 CC Query Match 17.0%; Score 996; DB 1; Length 491;
 CC Best Local Similarity 45.6%; Pred. No. 1.9e-45;
 CC Matches 204; Conservative 81; Mismatches 156; Indels 6; Gaps 4;
 CC -----
 CC QY 29 FKILVANRGEIAVRAFAALETGAATVAIYPRDRGSRFSPASPAVRIGTEGSPVKAY 88
 CC Db 2 FSKILVANRGEIAIRVMRARELGKISVAVSEADKNALFTRVADRAYEIG-KPAPSQSY 60
 CC QY 89 LDIDEITGAKKVADAIYPGYGFLENQAQARECAENGITFTGPTPEVLDLTGDKSRV 148
 CC Db 61 LRIDRILEVAEKAGAEIHPGYFLAENPRLGECEKQIKLPGKSGVTEAMGDKITS 120
 CC QY 149 TAAKAGLPLVABSTPS-KNIDIVKSAEQTPYIPFVAVAGGGGRMRFVSSPDELRL 207
 CC Db 121 KLKMGAGVPVPGTDOGVSDPDEAARIADISGIVPVIKASAGGGGIMRAVYEEDELIRA 180
 CC QY 208 ATEASREAAFGDGSVYVERAVINPQHIEVQILGDRTEGVHLYERDCSLQRRHQVVE 267
 CC Db 181 MESTQSVAAAFGDPVTYIEKYLEPRHTEFQVMADESQVNIHLADRECSIQRRHQKLE 240
 CC QY 268 IAPAQHLDPELRICADAVKFCRSIGYOCAGTVEFLVDEKGNHVEIENPRTQVETHT 327
 CC Db 241 EAPSPIMTPELRMRGSAVKAAYEYIGYENAGTVEFLY-SNGDFYFLEMNTRIQVEHPIT 299
 CC QY 328 EEVTEVDLKAQMLAAGATLKBELGTQDKIKTHGAALQCRITTEDPNNGFRPDTGTITA 387
 CC Db 300 EVITGVDLVKEQIRVAGS---EELRTQKDNIRHGAIECRINAENPLADFAFPNPKKITG 356
 CC QY 388 YRSPGAGVYLDGAAQLGGEITAFHSDMLVKMTCRSGDFETAVARAQALAEFTVSGVAT 447
 CC Db 357 YRSPGGIGRVDSGVYNNYIPFPYDSMTSKLIVMGWMDROEAINRMKRALSEYIILGVKT 416
 CC QY 448 NIGFLRALREEDFTSKRIATGFIGDH 474
 CC Db 417 TIFPHKAIMNEAFRGELETHFVDEY 443

RESULT 11

ACCC_HAEIN

ID ACCC_HAEIN STANDARD; PRT; 448 AA.

AC P3873;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA
 DE carboxylase) [EC 6.4.1.2] (ACC).
 DE ACCC OR HI0972.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Spriggs T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RL Science 269:496-512(1995).
 CC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
 CC CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE
 CC CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE
 CC TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)
 CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
 CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
 CC -!- SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN
 CC CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS
 CC OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (BY SIMILARITY).
 CC -!- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-
 CC PHOSPHATE SYNTHETASES.
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 CC -----
 CC EMBL: U32778; AAC22632.1; -
 CC DR PIR: F64105; F64105.
 CC DR HSP: P24182; IBNC.
 CC DR TIGR: HI0972; -
 CC DR InterPro: IPR004549; AccC.
 CC DR InterPro: IPR005482; Biotin_carb_C.
 CC DR InterPro: IPR005479; CPhase_L_D2.
 CC DR InterPro: IPR005481; CPhase_L_N.
 CC DR Pfam: PF02785; Biotin_carb_C; 1.
 CC DR Pfam: PF02786; CPhase_L_D2; 1.
 CC DR TIGRFAMs: TIGR00514; accC; 1.
 CC DR PROSITE: PS00866; CPSASE_1; 1.
 CC DR PROSITE: PS00867; CPSASE_2; 1.
 CC KW Fatty acid biosynthesis; Ligase; Biotin; ATP-binding;
 CC Complete proteome.
 CC FT NP_BIND 163 168 ATP (POTENTIAL).
 CC FT ACT_SITE 292 292 POTENTIAL.
 CC SQ SEQUENCE 448 AA; 49108 MW; 2B497E2A31ED96D1 CRC64;
 CC -----
 CC Query Match 16.2%; Score 950; DB 1; Length 448;
 CC Best Local Similarity 48.3%; Pred. No. 4.5e-43;
 CC Matches 212; Conservative 57; Mismatches 152; Indels 18; Gaps 9;
 CC -----

QY 30 KKLIVANRGEIAVRAFAALETGAATVAIYPRDRGSRFSPASPAVRIGTEGSPVKAYL 89

Db 3 EKVIANRGEIALRIILRACKELGKIVAVSHVSTADRLKHLVLADEFTICIGPAPS-AKSYL 61

QY 90 DIDEITGAKKVADAIYPGYGFLENQAQARECAENGITFTGPTPEVLDLTGDKSRV 149


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FT HELIX 34 36
FT TURN 37 38
FT HELIX 40 44
FT STRAND 47 52
FT HELIX 56 58
FT TURN 59 61
FT HELIX 63 73
FT TURN 74 74
FT STRAND 77 79
FT TURN 84 87
FT HELIX 89 97
FT TURN 98 99
FT STRAND 101 102
FT HELIX 107 114
FT TURN 116 125
FT TURN 126 127
FT STRAND 130 130
FT STRAND 133 133
FT HELIX 142 152
FT STRAND 156 160
FT STRAND 172 172
FT HELIX 175 188
FT STRAND 200 202
FT STRAND 208 217
FT TURN 222 234
FT TURN 235 236
FT STRAND 237 243
FT TURN 246 247
FT HELIX 250 267
FT TURN 268 268
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FT STRAND 283 290
FT TURN 295 296
FT HELIX 297 304
FT HELIX 308 316
FT TURN 317 318
FT HELIX 325 327
FT STRAND 333 340
FT STRAND 342 342
FT TURN 344 346
FT STRAND 349 349
FT STRAND 352 353
FT STRAND 356 358
FT TURN 363 364
FT STRAND 365 368
FT TURN 373 374
FT STRAND 376 377
FT STRAND 384 392
FT HELIX 395 408
FT STRAND 410 412
FT HELIX 418 425
FT TURN 426 426
FT HELIX 428 432
FT TURN 437 438
FT HELIX 439 444
FT TURN 445 445
SQ SEQUENCE 449 AA; 49320 MW; 68C55FT10ACB4F170 CRC64;

Query Match
Best Local Similarity 16.0%; Score 940; DB 1; Length 449;
Matches 203; Conservative 66; Mismatches 155; Indels 10; Gaps 6;

QY 31 KILVANGETIAVAFRAALETGAATVAIYREDRGSFHSFAEAVRICTEGSPVKAYLD 90
    ||:|||||: || |||||: || |||||: || |||||: || |||||:
4 KIVIANGETIALRILRACKELGKTVAVHSSADRLDKHLLADETVCIGPAPS-VKSYLN 62
    ||:|||||: || |||||: || |||||: || |||||: || |||||:
91 IDEIIGAAKKVADAIYPCYGLSENQAQLARECAENGITFIPTPEVLDLTGDKRAVTA 150
    || ||||: || ||||: || ||||: || ||||: || ||||: || ||||:
63 IPAIIISAAITGAVALHPYGLSENANFAEQVRSQGFIFGPKAETIRLMGDKVSAIAA 122
    || ||||: || ||||: || ||||: || ||||: || ||||: || ||||:
QY 151 AKKAGLPVLAETPSKNIDDIKVS---AEGQYPIFVKAVAGGGGMRFEVSSPDRLKL 207
    ||||: || ||||: || ||||: || ||||: || ||||: || ||||:

```

```

Db 123 MKKAGVPCVPGSDGPLG-DDMDKNRAIAKRIGYPVLIKASGGGGGRGMRVVRGDAELAQS 181
QY 208 ATEASREAEAFGDGVSYYVERAVINPOHLEVOILGDRTGEVHLXERDCSLORRHOKVVE 267
Db 182 ISWTRAEAKAFSNDVMYMEKYLENPRHVEIOVLADGQGNAILYLAERDCSMORRHKVVE 241
QY 268 IAPQHLDPRLDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFIEHNPRIQVEHVT 327
    ||| : ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 EAPAGGITPELRRYIGERCACAKVDIGYRGAGTFFELF-ENGEEFYIEMNTRIQVEHPT 300
    ||| : ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 328 EEVTEVDLVKAQMRILAAGATLKELGITQDKIKTHGAALOCRTTDPNNGFRPDTGTIA 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 EMITGVLLIKELRIAAAG--QPLSIKQBEVHVRGHAECRIINAEDPNT-FLPSPKIIIR 356
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 388 YRSPGGAGVRLDGAAGLGEITAHFDSMLVKMTCRGSDFETAVARAORALAEFTVSGVAT 447
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 357 FHAPGGFGVRWESHYAGYTPPYDSMIGKLCICGENRDVAIAKMKALQELIIDGIKT 416
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 448 NIGFLRALREEDF 461
    || : ||: ||
Db 417 NVDLQIRIMNDENF 430

RESULT 13
ACCC_FCO57 STANDARD; PRT; 449 AA.
AC Q8X9B6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA
DE carboxylase) (EC 6.4.1.2) (ACC).
GN ACCC OR Z4616 OR ECS4128.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grothbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tohe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
CC CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE
CC CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE
CC TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA.
CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + Co(2)
CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
CC -!- PATHWAY: long-chain fatty acid biosynthesis; first step.
CC -!- SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN
CC CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS
CC OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-
CC PHOSPHATE SYNTHETASES.
CC -----

```


Db 3 EVLIANRGEIALRILRACKELGKIKTAVHSTADRELMLSLADESVCLG-PAPATQSVL 61
 QY 90 DIDEILGAKKVADAIIPGYGFLSENAQLARECAENGITFGTPEVLDTLDCDSRAVT 149
 Db 62 QPALIAAAAEVGTATIHGPGFLAENADFAEQIERSGFTFGVTAETIRLMGDKVSAD 121
 QY 150 AAKKAGLPVL--AETPSKNIDDIIVKSAEGQYPIFVKAVAGGGRGMRVSSPDELRL 207
 Db 122 AMKRAGVPVPSDGLPEDEETALAIAREVCYPIVKAAGGGGRGMRVYVDESELKS 181
 QY 208 ATEASREAAFGDGSVYVERAVINPQIEVILGDRTEGVVHLVYERDCSLQRHKKVVE 267
 Db 182 AKLIRTEAGAAFGNPMVILEKLTINPRHVEVQVLSGQGNATHLGDRCSLQRHKKVIE 241
 QY 268 IAPACHLDELPRICADACAKFCRSIGYOGAGTVEFLVDEKGNHVFEMNPIQVHEVT 327
 Db 242 EPAPGIDKAEQVFAFCVQACIEIGYAGAGTFEFLY-ENGRFYFIEMNTRVQVHEPVS 300
 QY 328 EEVTEVDVLKQAMRLAAGATLKLGLTODKIKTHGAALQCRITTEDPNNNGFRPDTGTTA 387
 Db 301 EMVIGVDIVKEMRIASG--EKLIRQEDVVIRGHALECRINAEDPKT-FMPSFGKYKH 356
 QY 388 YSPGAGVRLDGAQLGEGITTAHDSMLVKTGCRGSDPETAVARAQALABFTVSGVAT 447
 Db 357 FHAPGGNGYRVDSHLVSGYSVPNYDSLGVKVTYTGADRDALARMNALDELIVDGK 416
 QY 448 NIGFLRALREEDF 461
 Db 417 NTELKDLVRDAAF 430

RESULT 15

MCCA.HUMAN
 ID MCCA.HUMAN STANDARD; PRT; 725 AA.
 AC Q96RQ3; Q9H959; Q9NS97;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
 DE (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha
 DE subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit).
 GN MCCC1 OR MCCA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANTS MCGI ARG-325 AND SER-385.
 RX PubMed-11170888;
 RA Gallardo M.E., Desviat L.R., Rodriguez J.M., Esparza-Gordillo J.,
 RA Perez-Cerda C., Perez B., Rodriguez-Pombo P., Criado O., Sanz R.,
 RA Morton D.H., Gibson K.M., Le T.P., Ribes A., Rodriguez de Cordoba S.,
 RA Ugarte M., Penalva M.A.;
 RT "The molecular basis of 3-methylcrotonylglycinuria, a disorder of
 RT leucine catabolism.";
 RL Am. J. Hum. Genet. 68:334-346(2001).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT HIS-464.
 RX MEDLINE-21295033; PubMed-11401427;
 RA Obata K., Fukuda T., Morishita R., Abe S., Asakawa S., Yamaguchi S.,
 RA Yoshino M., Ihara K., Murayama K., Shigemoto K., Shimizu N., Kondo I.;
 RT "Human biotin-containing subunit of 3-methylcrotonyl-CoA carboxylase
 RT gene (MCCA): cDNA sequence, genomic organization, localization to
 RT chromosomal band 3q27, and expression.";
 RL Genomics 72:145-152(2001).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT MCGI PHE-535.
 RX MEDLINE-21299419; PubMed-11406611;
 RA Holzinger A., Roeschinger W., Lagler F., Mayerhofer P.U., Lichtner P.,
 RA Kattenfeld T., Thuy L.P., Nyhan W.L., Koch H.G., Muntau A.C.,
 RA Roscher A.A.;
 RT "Cloning of the human MCCA and MCCB genes and mutations therein reveal

the molecular cause of 3-methylcrotonyl-CoA: carboxylase
 deficiency.";
 Hum. Mol. Genet. 10:1299-1306(2001).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS MCGI VAL-289; SER-385; PRO-437 AND
 RP HIS-532.
 RX PubMed-11181649;
 RA Baumgartner M.R., Almashanu S., Suormala T., Obie C., Cole R.N.,
 RA Packman S., Baumgartner E.R., Valle D.;
 RT "The molecular basis of human 3-methylcrotonyl-CoA carboxylase
 RT deficiency.";
 RL J. Clin. Invest. 107:495-504(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Isozaki T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
 RA Matsumura H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
 RA Nakamura Y., Nagahara K., Masuho Y., Sasaki N.;
 RT "NED0 human cDNA sequencing project.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE-22388257; PubMed-12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3)(-) = ADP +
 CC phosphate + 3-methylglutaconyl-CoA.
 CC -!- COFACTOR: Biotin.
 CC -!- PATHWAY: Leucine catabolism.
 CC -!- SUBUNIT: Probably a dodecamer composed of six biotin-containing
 CC alpha subunits and six beta subunits.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -!- DISEASE: Defects in MCCC1 are the cause of 3-
 CC methylcrotonylglycinuria type I (MCGI) [MIM:210200]; also
 CC designated CGA or CG2. MCGI is a recessive disease that is
 CC characterized by muscular hypotonia and atrophy, probably of
 CC spinal origin.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF310972; RA653095.1; -
 DR EMBL; AB029826; BA99407.1; -
 DR EMBL; AF297332; AAK67986.1; -
 DR EMBL; AF310339; RA650245.1; -
 DR EMBL; AK023051; BAB14377.1; -
 DR EMBL; BC004214; AAH04214.1; -
 DR EMBL; BC004187; AAH04187.1; -
 DR Genbank; HGNC:6936; MCCC1.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 15:51:28 : Search time 89.6587 Seconds
(without alignments)
3330.038 Million cell updates/sec

Title: US-09-974-973A-2
Perfect score: 5665
Sequence: 1 MIAITGLLLKGIITLVST.....RVVVPAAATKVEGDLIVVVS 1157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL.23:*
- 1: sp.archaea.*
 - 2: sp.bacteria.*
 - 3: sp.fungi.*
 - 4: sp.human.*
 - 5: sp.invertebrate.*
 - 6: sp.mammal.*
 - 7: sp.mhc.*
 - 8: sp.organelle.*
 - 9: sp.phage.*
 - 10: sp.plant.*
 - 11: sp.rodent.*
 - 12: sp.virus.*
 - 13: sp.vertibrate.*
 - 14: sp.unclassified.*
 - 15: sp.virus.*
 - 16: sp.bacteriapi.*
 - 17: sp.archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5772	98.4	1140	2 Q8L2G4	Q8L2G4 corynebacte
2	5759	98.2	1140	16 O54587	O54587 corynebacte
3	5322	90.7	1168	16 Q8FRQ0	Q8FRQ0 corynebacte
4	5297.5	90.3	1139	2 Q8RQL2	Q8RQL2 corynebacte
5	3797	64.7	1124	16 Q9RK64	Q9RK64 streptomyc
6	3786.5	64.6	1127	2 Q9F843	Q9F843 mycobacteri
7	3713.5	63.3	1127	16 P95127	P95127 mycobacteri
8	3484	59.4	1124	2 Q50450	Q50450 mycobacteri
9	2550.5	43.5	1178	13 Q8JHF6	Q8JHF6 gallus gall
10	2535.5	43.2	1150	16 Q9K9M0	Q9K9M0 bacillus su
11	2530	43.1	1148	16 Q9KWU4	Q9KWU4 bacillus su
12	2523.5	43.0	1180	13 Q9DPT1	Q9DPT1 brachydanio
13	2509	42.8	1147	2 P94448	P94448 bacillus st
14	2507.5	42.8	1192	3 Q9HES8	Q9HES8 aspergillus
15	2494	42.5	1146	16 Q8Y846	Q8Y846 listeria mo
16	2491	42.5	1146	16 Q92CW1	Q92CW1 listeria in

Q97fr7 clostridium
Q8nx69 staphylococ
Q99uy8 staphylococ
Q93918 aspergillus
Q8fyt0 brucella su
Q8ubx3 agrobacteri
Q88f27 rhizobium l
Q8ayn3 pagrus majo
Q8yJ20 brucella me
Q8cpm3 staphylococ
Q17732 caenorhabdi
Q9nuel schizosacch
Q9x000 drosophila
P78822 schizosacch
Q8xlt3 pichia angu
Q92113 rhizobium m
Q8mkw5 drosophila
Q16921 aedes aegypt
Q8er83 oceanobacil
Q9chq7 lactococcus
Q9rat6 lactococcus
Q59740 rhizobium e
Q8axq6 pagrus majo
Q9xbj1 bacillus ce
Q62043 mus musculu
Q9kxw5 bacillus su
Q8bp54 mus musculu
Q8mkw4 drosophila
Q8mkw3 drosophila

ALIGNMENTS

RESULT 1

ID Q8L2G4 PRELIMINARY; PRT; 1140 AA.
AC Q8L2G4;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Pyruvate carboxylase.
GN PYC.
OS Corynebacterium crenatum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=168810;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD945;
RA Wang J., Ding J., Liu Y.;
RT "Cloning and Expression of Pyruvate Carboxylase Gene in
RT Corynebacterium crenatum CD945.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF503915; AM27458.1; -;
DR InterPro; IPR001882; Biotin_attach.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; Cphase_L.D2.
DR InterPro; IPR005481; Cphase_L.N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR Pfam; PF00289; CPhase_L_chain; 1.
DR Pfam; PF02786; CPhase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRfams; TIGR01235; pyruv_carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPhase_2; 1.
SQ SEQUENCE 1140 AA; 123126 MW; FFA90BB7644C910E CRC64;

Query Match 98.4%; Score 5772; DB 2; Length 1140;
 Best Local Similarity 99.6%; Pred. No. 3 4e-300;
 Matches 1135; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 18 VSTHTSSTLPAPFKKILVANRGEIAVAFRAALETGAATVAIYPRDRGSHFHSFASEAVR 77
 DB 1 MSTHTSSTLPAPFKKILVANRGEIAVAFRAALETGAATVAIYPRDRGSHFHSFASEAVR 60

QY 78 IGTEGSPVKAYLIDIELGAKKVKADAIYPGVGFLSENAQLARECAENGITFIGTPEV 137
 DB 61 IGTEGSPVKAYLIDIELGAKKVKADAIYPGVGFLSENAQLARECAENGITFIGTPEV 120

QY 138 LDLTGDKSRVTAACKAGLPLVAESTPSKNIDIVKSAEGQTIPIFVKAVAGGGGGRMF 197
 DB 121 LDLTGDKSRVTAACKAGLPLVAESTPSKNIDIVKSAEGQTIPIFVKAVAGGGGGRMF 180

QY 198 VSSPDELRLKLAETASREAAAGDGSVYVERAVINPQHIEVQLIGRTGEVHLYERDCS 257
 DB 181 VSSPDELRLKLAETASREAAAGDGSVYVERAVINPQHIEVQLIGRTGEVHLYERDCS 240

QY 258 LQRRHOKVVEIAPAOLHDELDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEWN 317
 DB 241 LQRRHOKVVEIAPAOLHDELDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEWN 300

QY 318 PRIQVEHTVTEVEVDLVKAQMLAAGATLKLGLTQDKIKITHGAALQCRITTEDPNNG 377
 DB 301 PRIQVEHTVTEVEVDLVKAQMLAAGATLKLGLTQDKIKITHGAALQCRITTEDPNNG 360

QY 378 FRPDGTITAYRSPGAGVRLDGAOLGGEITAHFDSMLVKMTCRGSDFTAVARAQAL 437
 DB 361 FRPDGTITAYRSPGAGVRLDGAOLGGEITAHFDSMLVKMTCRGSDFTAVARAQAL 420

QY 438 AEFTVSGVATNIGFLRALREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYADV 497
 DB 421 AEFTVSGVATNIGFLRALREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRILDYADV 480

QY 498 TVNKHGVPKDVAPIDKLPNIKDLPLPRGSRDLKQLGPAFAFARLREQDALAVDTDT 557
 DB 481 TVNKHGVPKDVAPIDKLPNIKDLPLPRGSRDLKQLGPAFAFARLREQDALAVDTDT 540

QY 558 FRAHQSLIATVRFSFALPAAEAVALKTPILLSVEANGGATYDVAMRFLFDPDRDLDE 617
 DB 541 FRAHQSLIATVRFSFALPAAEAVALKTPILLSVEANGGATYDVAMRFLFDPDRDLDE 600

QY 618 LREAMPNVNIQMLLRGNTVGTTPYDPSVCRAFVKEAASGVYDIFRIFDALNDVSMRPA 677
 DB 601 LREAMPNVNIQMLLRGNTVGTTPYDPSVCRAFVKEAASGVYDIFRIFDALNDVSMRPA 660

QY 678 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYILKMAEETVKSAGHILAKDMAGLLR 737
 DB 661 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYILKMAEETVKSAGHILAKDMAGLLR 720

QY 738 PAAVKLTALRREFDLPVHVHTHTAGGOLATYFAAQAQADAVDGSAPLSGTTSDPS 797
 DB 721 PAAVKLTALRREFDLPVHVHTHTAGGOLATYFAAQAQADAVDGSAPLSGTTSDPS 780

QY 798 LSAIYAFAHTRDRDGLSLEAVSDLEPYEAVRGLYLPFESGTPGPTGRVYRHEIPGGOL 857
 DB 781 LSAIYAFAHTRDRDGLSLEAVSDLEPYEAVRGLYLPFESGTPGPTGRVYRHEIPGGOL 840

QY 858 SNLRAQATGLADREFELIEDNVAVNEMLGPTKVTSPSSKVVGDIALHLVAGVDPADF 917
 DB 841 SNLRAQATGLADREFELIEDNVAVNEMLGPTKVTSPSSKVVGDIALHLVAGVDPADF 900

QY 918 AADPKQYIDIPDSVIAFLRGELGNPPGWPPEPLRTRALGRSGKAPLFEVPEEQAHLLDA 977
 DB 901 AADPKQYIDIPDSVIAFLRGELGNPPGWPPEPLRTRALGRSGKAPLFEVPEEQAHLLDA 960

QY 978 DSKERRNSLNLLFPKPTPEEFLEHRRRFGNTSALDDREFFYGLVGEHRETLRLRDLVTRP 1037
 DB 961 DSKERRNSLNLLFPKPTPEEFLEHRRRFGNTSALDDREFFYGLVGEHRETLRLRDLVTRP 1020

QY 1038 LLVRLDAISEPDDKGMNVVAVNGOIRPMRVDRSVESTATAEKADSSNKGHVAAPFA 1097
 DB 1021 LLVRLDAISEPDDKGMNVVAVNGOIRPMRVDRSVESTATAEKADSSNKGHVAAPFA 1080

QY 1098 LVVTVTVAEDEVKAGDAVAIIEMKMEATITASVDGKIERVVVPAATKVEGDLIVVVS 1157
 DB 1081 GVVTVTVAEDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAAATKVEGDLIVVIS 1140

RESULT 2
 054587 PRELIMINARY; PRT; 1140 AA.
 AC 054587;
 DT 01-JUN-1998 (TEMBLrel. 06, Created)
 DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Pyruvate carboxylase (EC 6.4.1.1).
 GN PYC OR CGL0689.
 OS Corynebacterium glutamicum (Brevibacterium flaviu).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=21253;
 RA Koffas M.A.G., Ramamoorthi R., Pine W.A., Sinsky A.J.,
 RA Stephanopoulos G.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032;
 RA Peters-Wendisch P.G., Kreutzer C., Kalinowski J., Patek M., Sahn H.,
 RA Eikmanns B.J.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RL "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- COFACTOR: BIOTIN (BY SIMILARITY).
 DR EMBL; AF038548; AAB92588.1; -;
 DR EMBL; Y09548; CAA70739.1; -;
 DR EMBL; AF005276; BAB98082.1; -;
 DR HSSP; P24182; 1BNC.
 DR InterPro; IPR001882; Biotin_attach.
 DR InterPro; IPR005482; Biotin_carb_C.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR InterPro; IPR005479; CPase_L_D2.
 DR InterPro; IPR005481; CPase_L_N.
 DR InterPro; IPR000891; HMGL-like.
 DR InterPro; IPR003379; PYC_OADA.
 DR InterPro; IPR005930; Pyruv_carbox.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF00364; Biotin_lipoyl; 1.
 DR Pfam; PF00289; CPase_L_chain; 1.
 DR Pfam; PF02786; CPase_L_D2; 1.
 DR Pfam; PF00682; HMGL-like; 1.
 DR Pfam; PF02436; PYC_OADA; 1.
 DR TIGRfams; TIGR01235; Pyruv_carbox; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 DR PROSITE; PS00867; CPASE_2; 1.
 KW Biotin; Ligase; Pyruvate; Complete proteome.
 SQ SEQUENCE 1140 AA; 123102 MW; 2A6D4B4ED2FEB531 CRC64;

Query Match 98.2%; Score 5759; DB 16; Length 1140;
 Best Local Similarity 99.4%; Pred. No. 1.7e-29;
 Matches 1133; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 18 VSTHTSSTLPAPFKKILVANRGEIAVAFRAALETGAATVAIYPRDRGSHFHSFASEAVR 77
 DB 1 MSTHTSSTLPAPFKKILVANRGEIAVAFRAALETGAATVAIYPRDRGSHFHSFASEAVR 60

QY 78 IGTEGSPVKAYLDIDELIIGAAKKVKADAIYPCYGFSLSENAQLARCAENGITFIPTPEV 137
DB 61 IGTEGSPVKAYLDIDELIIGAAKKVKADAIYPCYGFSLSENAQLARCAENGITFIPTPEV 120
QY 138 LDLTGDKSRVTAANKAGLPVLAESTPSKNIDDIIVKSABGGTYPIFVKAVAGGGRGMRP 197
DB 121 LDLTGDKSRVTAANKAGLPVLAESTPSKNIDDIIVKSABGGTYPIFVKAVAGGGRGMRP 180
QY 198 VSPDELKRLATFASREAAAGDGSVYVERAVINPOHIEVOILGDRTGEVHLVERDCS 257
DB 181 VASPDLEKRLATFASREAAAGDGSVYVERAVINPOHIEVOILGDRTGEVHLVERDCS 240
QY 258 LQRRHQKVVEIAPAOHLDELDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEKN 317
DB 241 LQRRHQKVVEIAPAOHLDELDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEKN 300
QY 318 PRIQVEHTVTEVTEVDLVKAQMLAAGATLTKELGLTQDKIKTHGAALQCRITTEDPNNG 377
DB 301 PRIQVEHTVTEVTEVDLVKAQMLAAGATLTKELGLTQDKIKTHGAALQCRITTEDPNNG 360
QY 378 FRPDTGTITAYRSPGAGVRLDGAOLGGEITTAHFDPSMLVKMTCRGSDFETAVARAQAL 437
DB 361 FRPDTGTITAYRSPGAGVRLDGAOLGGEITTAHFDPSMLVKMTCRGSDFETAVARAQAL 420
QY 438 ABFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDDQGRILDYADV 497
DB 421 ABFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDDQGRILDYADV 480
QY 498 TVNKHGVRPKDVAAPIDKLPNIKDLPLPRGSRDLKQLGPAFAFARDLREQDALAVTDIT 557
DB 481 TVNKHGVRPKDVAAPIDKLPNIKDLPLPRGSRDLKQLGPAFAFARDLREQDALAVTDIT 540
QY 558 FDAHQSLATRVSPALPAAEVAKLTPELLSVEAWGATYDVAMRFLFEDPMDRLDE 617
DB 541 FDAHQSLATRVSPALPAAEVAKLTPELLSVEAWGATYDVAMRFLFEDPMDRLDE 600
QY 618 LREAMPNVNIQMLLRGNTVGTYPDSVCRAFVKEAASGVVDIFRIFDALNDVSQMRPA 677
DB 601 LREAMPNVNIQMLLRGNTVGTYPDSVCRAFVKEAASGVVDIFRIFDALNDVSQMRPA 660
QY 678 IDAVLENTNVAEVAAMAYSGDLSDPNEKLYTLDYILKMAEEIVKSAHILAKDMAGLLR 737
DB 661 IDAVLENTNVAEVAAMAYSGDLSDPNEKLYTLDYILKMAEEIVKSAHILAKDMAGLLR 720
QY 738 PAAVTKLVTLRREFDLPVHVHTHTAGGOLATYFAAAQAGADAVDGSAPLSGTTSQPS 797
DB 721 PAAVTKLVTLRREFDLPVHVHTHTAGGOLATYFAAAQAGADAVDGSAPLSGTTSQPS 780
QY 798 LSAIVAFAHTRDRTGLSLVLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 857
DB 781 LSAIVAFAHTRDRTGLSLVLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 840
QY 858 SNLRAQATLGLADREFELIEDNYAANEMLGRPTKVTSPSKVVGDLALHLVAGVDPADF 917
DB 841 SNLRAQATLGLADREFELIEDNYAANEMLGRPTKVTSPSKVVGDLALHLVAGVDPADF 900
QY 918 AADPQKYDIPDSVIAFLRGLNPPGWPPELTRALEGRSEKAPLITEVPEEQAHDLA 977
DB 901 AADPQKYDIPDSVIAFLRGLNPPGWPPELTRALEGRSEKAPLITEVPEEQAHDLA 960
QY 978 DSKERRNSUNRLLFPKPTPEEFLEHRRRFGNTSALDDREFYGLVREGRETLIRLPDVRTP 1037
DB 961 DSKERRNSUNRLLFPKPTPEEFLEHRRRFGNTSALDDREFYGLVREGRETLIRLPDVRTP 1020
QY 1038 LVLRLDAISPDDKGMNVVANYNGQIRPMRVDRSVESVTATAEAKADSNKGNHVAAPFA 1097
DB 1021 LVLRLDAISPDDKGMNVVANYNGQIRPMRVDRSVESVTATAEAKADSNKGNHVAAPFA 1080
QY 1098 GVVTVTVAGDEVKAGDAVAIEAMKMEATITASVDGKIERYVVVPAATKVEGGDLIVVVS 1157
DB 1081 GVVTVTVAGDEVKAGDAVAIEAMKMEATITASVDGKIERYVVVPAATKVEGGDLIVVVS 1140

RESULT 3
Q8FRQ0 PRELIMINARY; PRT; 1168 AA.
AC Q8FRQ0;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1).
GN PYC OR CE0709.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005216; BAC17519.1; -
KW Ligase; Complete proteome.
SQ SEQUENCE 1168 AA; 126245 MW; A5D5A4DD4DF285F8 CRC64;
Query Match 90.7%; Score 5322; DB 16; Length 1168;
Best Local Similarity 90.8%; Pred. No. 4.1e-276;
Matches 1041; Conservative 46; Mismatches 57; Indels 2; Gaps 2;
QY 12 KGITLVSTHTSTLPFAFKKILVANGETAVRAFALETGAATVAIYPREDGSRHSF 71
DB 25 KGTKTIVTWT-TPSTLPFAFKKILVANGETAVRAFALETGAATVAIYPREDGSRHSF 83
QY 72 ASEAVRIGTEGSPVKAYLDIDELIIGAAKKVKADAIYPCYGFSLSENAQLARCAENGITFI 131
DB 84 ASEAVRIGTEGSPVKAYLDIDELIIGAAKKVKADAIYPCYGFSLSENAQLARCAENGITFI 143
QY 132 GTPTEVIDLTGDKSRVTAANKAGLPVLAESTPSKNIDDIIVKSABGGTYPIFVKAVAGG 191
DB 144 GTPTEVIDLTGDKSRVTAANKAGLPVLAESTPSKNIDDIIVKSABGGTYPIFVKAVAGG 203
QY 192 GRCMRVSPDELRKLATFASREAAAGDGSVYVERAVINPOHIEVOILGDRTGEVHL 251
DB 204 GRCMRVSPDELRKLATFASREAAAGDGSVYVERAVINPOHIEVOILGDRTGEVHL 263
QY 252 YERDCSLORRHQKVVEIAPAOHLDELDRICADAVKFCRSIGYOGAGTVEFLVDEAGNH 311
DB 264 YERDCSLORRHQKVVEIAPAOHLDELDRICADAVKFCRSIGYOGAGTVEFLVDEAGNH 323
QY 312 VFTEMNPRIQVEHTVTEVTEVDLVKAQMLAAGATLTKELGLTQDKIKTHGAALQCRIT 371
DB 324 VFTEMNPRIQVEHTVTEVTEVDLVKAQMLAAGATLTKELGLTQDKIKTHGAALQCRIT 383
QY 372 EDNNFRPDTGTITAYRSPGAGVRLDGAOLGGEITTAHFDPSMLVKMTCRGSDFETAVA 431
DB 384 EDPSNFRPDTGTITAYRSPGAGVRLDGAOLGGEITTAHFDPSMLVKMTCRGSDFETAVA 443
QY 432 RAQRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRIL 491
DB 444 RAQRALAEFTVSGVATNIGFLRALLREEDFTSKRIATGFIGDHPHLLQAPPADDEQGRIL 503
QY 492 DYLAADVTVNKHGVRPKDVAAPIDKLPNIKDLPLPRGSRDLKQLGPAFAFARDLREQDAL 551
DB 504 EYLADADVTVNKHGVRPKDVAAPIDKLPNIKDLPLPRGSRDLKQLGPAFAFARDLREQDAL 562
QY 552 AVTDTTFRDQHSLLATRVESFALKPAAEVAKLTPELLSVEAWGATYDVAMRFLFEDP 611
DB 563 AVTDTTFRDQHSLLATRVESFALKPAAEVAKLTPELLSVEAWGATYDVAMRFLFEDP 622
QY 612 WDRLDELREAMPNVNIQMLLRGNTVGTYPDSVCRAFVKEAASGVVDIFRIFDALNDV 671
DB 623 WARLDELREAMPNVNIQMLLRGNTVGTYPDSVCRAFVKEAASGVVDIFRIFDALNDV 682

QY	672	SOMRPAIDAVLENTTAAVEAMAYSGDLSDPNPKLYTLDYLYLKMAEEIVKSGAHILAIKD	731
Db	683	SOMRPAIDAVLETTGTVAAVEAMAYSGDLSNPGSKLYTLDYLLALBPQIVDSGAHILAIKD	742
QY	732	MAGLLPAAATKLVTLALREFDLPVHVHTDTAGGOLATVFAAAQAGADAVDGSAPLSG	791
Db	743	MAGLLPAAATKLVTLALREFDLPVHVHTDTAGGOLATVYLAANAAGADAVDAASAPLSG	802
QY	792	TTSQPSLSATVAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFFSGTGPPTGRVYRHE	851
Db	803	TTSQPSKSLVAFAHTRRDTGLNLQAVSDLEPYWEAVRGLYLPFFSGTGPPTGRVYRHE	862
QY	852	IPGQLSNLRQAOTALGLADRFELIDENYAAVNMELGRPTKVPSSKVVYGDIALHLVGAG	911
Db	863	IPGQLSNLRQAVALGLADRFELIEDYAAVNMELGRPTKVPSSKVVYGDIALHLVGAG	922
QY	912	VDPADFAADPKYDIPDSVIAFIRLGBELNPGPGWPEPLRTRALEGRSEKAPITEVPEEE	971
Db	923	VSPEDFAADPKYDIPDSVIAFIRLGBELTTPPGGWPEPLRTRALEGRSQKAPLAEIPAEE	982
QY	972	QAHLDADDSEKERNLSNRLIFPKPTFEFLBHRFRFGNTSALDDREFFYGLVGEVRETLIRL	1031
Db	983	QAHLDSDSSERRGTLNRLIFPKPTFEFLBHRFRFGNTSALDDREFFYGLVGEVRETLIRL	1042
QY	1032	PDYRTPLLYRLDAISEPDDKMRNVVANVNGQIRPKRVDRSYESVTATAEKADSNKKGH	1091
Db	1043	TGVSTPMVVRDLAVSEPDGKMRNVVNVNGQIRPKRVDRSYESVTATAEKADATNKGH	1102
QY	1092	VAAPFGAGVTVTVAEGDEVKAGDAVALIEAMKMEATITASVDGKIEVVVYPAATKVEGGD	1151
Db	1103	VAAPFGAGVTVTVAEGDEIRKAGDAVALIEAMKMEATITAPDVGVIDRVVYPAATKVEGGD	1162
QY	1152	LIVVVS 1157	
Db	1163	LIVVVS 1168	

RESULT 4

Q8RQL2	ID	Q8RQL2	PRELIMINARY;	PRT;	1139	AA.
AC	DT	AC	Q8RQL2;			
DT	01-JUN-2002	(TREMBLrel. 21, Created)				
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)				
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)				
DE	Pyruvate carboxylase.					
GN	pyc.					
OS	Corynebacterium efficiens.					
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;					
OC	Corynebacterineae; Corynebacteriaceae; Corynebacterium.					
OX	NCBI_TaxID=152794;					
EN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Akiyoshi N., Nonaka G., Kimura E., Kawahara Y., Sugimoto S.;					
RT	"Corynebacterium efficiens pyruvate carboxylase (pyc) gene, complete					
RL	CDS."					
RL	Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.					
CC	-1- COFATOR: BIOTIN (BY SIMILARITY).					
DR	EMBL; AB083239; BA888903.1; -					
DR	InterPro; IPR001882; Biotin_attach.					
DR	InterPro; IPR005482; Biotin_carb_C.					
DR	InterPro; IPR000089; Biotin_lipoyl.					
DR	InterPro; IPR005479; CPhase_L_D2.					
DR	InterPro; IPR005481; CPhase_L_N.					
DR	InterPro; IPR000891; HMGL-like.					
DR	InterPro; IPR003379; PYC_OADA.					
DR	InterPro; IPR005930; Pyruv_carbox.					
DR	Pfam; PF02785; Biotin_carb_C; 1.					
DR	Pfam; PF00364; biotin_lipoyl; 1.					
DR	Pfam; PF00289; CPhase_L_chain; 1.					
DR	Pfam; PF02786; CPhase_L_D2; 1.					
DR	Pfam; PF00682; HMGL-like; 1.					
DR	Pfam; PF02436; PYC_OADA; 1.					
DR	TIGRFAMS; TIGR01235; pyruv_carbox; 1.					

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QY 980 SKERRSNRLFLPKPTKEFLHRRRGNTSALDDREFFYGLVEGRETLIRLPDVRTPLL 1039
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 962 SAERGTGLNLEPKTEFELEHRRRGNTSALDDREFFYGLKEGREELIRLIGVSTPW 1021
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1040 VRLDASEDDKGMNVNANYNGOIRPMVRDRSVESVATAEKADSSNKGHVAAPFAGV 1099
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1022 VRLDAVSEDDKGMNVNANYNGOIRPMVRDRSVESVATAEKADATNKGHVAAPFAGV 1081
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1100 VTVTAEGDEKAGDAVAIEAMKMEATITASVDGKIERVVPAATKVEGGDLIVVVS 1157
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1082 VTVTAEGDEKAGDAVAIEAMKMEATITAPVDGVIDRVVPAATKVEGGDLIVVVS 1139
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
Q9RK64 PRELIMINARY; PRT; 1124 AA.
ID Q9RK64
AC Q9RK64;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Pyruvate carboxylase.
GN SCO0546 OR SCF11.26C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2); Harris D.;
RA Seeger K.J., Hopwood D.A.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Redenbach M., Kieser H.M., Denapaitte D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren D., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
RL EMBL; AL391105; CAB59603.1; -.
DR HSSP; P24182; 1BNC.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; Cfase_L_D2.
DR InterPro; IPR005481; Cphase_L_D2.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PVC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; Cpsase_L_chain; 1.

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DR Pfam; PF02786; Cpsase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGREMS; TIGR01245; pyruv_carbox; 1.
DR PROSITE; PS00867; Cpsase_2; 1.
KW complete proteome.
SQ SEQUENCE 1124 AA; 121071 MW; 1FEF4C4643954D31 CRC64;

Query Match 54.7%; Score 3797; DB 16; Length 1124;
Best Local Similarity 65.2%; Pred. No. 1.5e-194;
Matches 735; Conservative 156; Mismatches 227; Indels 10; Gaps 6;

QY 29 FKKILVANRGEIAVRAFAALETGAATVAIYPREDGSRHSFASBAVRIGTEGSPVKAY 88
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 FRKVLVANRGEIAIRAFAAGYELGARTVAVFPEDRNSLHRLKADRAYELGEGHPVAY 61
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 89 LDIDEIIGAAKYKADAIYPGYGFLSENAQIARECAENGITFTGPTPEVLDLTDGSKRAY 148
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 LSVEEIVRAARRAGADAVPYGYGFLSENPELACEEAGITFVGP SARILELTGNKARAY 121
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 149 TAAKKAGLPVLAESTPSTKNIDDIKSAEGQTYIFVKAVAGGGGRGMRFYSSPDELKLA 208
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 AAAREAGVPVIGSSAPSTDVDELVRAADDVGFVFKAVAGGGGRGMRVVEEPAQUREAI 181
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 209 TEASREAAAFGDSGVYVERAVINPOHIEVQIILGDRTEGVVHLYERDCSLQRHQKVEI 268
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 EAASREAAAFGDSGVYVERAVINPOHIEVQIILGDRTEGVVHLYERDCSLQRHQKVEI 241
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 269 APAQHLDPELRICADAVKFCRSIGYQGAGTVEFLVDEKGNHVFTEMNPRIQVEHTVTE 328
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 242 APAPNLDPALRRERICADAVNFAQIGYRNAGTVEFLVDRDGNHVFTEMNPRIQVEHTVTE 301
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 329 EVTEVDLVKAQMLAAGATILKELGLTQDKIKTHGAALQCRITTEDPNNGRPRDPTGITAY 388
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 302 EVTDVLDVSQLRIAGQTLADLAGAENITLRGAALQCRITTEDPNNGRPRDPTGITAY 361
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 389 RSPGGAGVRLLD-GAAQLGGEITAHFDSMLVKMTCRGSDFEFAVARAQLAAEFTVSGVAT 447
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 362 RSPGGSGIRLDGGTTHAGTEISAHFDLSMLVKLSRGDRFTTAVNRRARRAVERIRGVAT 421
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 448 NIGFLRALUREEDFTSKRTANGTIGDHPHLLQAPPADDEQGRILDLVADVYVKNPGRVPR 507
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 422 NIPFLQAVLDPPDFQAGRVVTSFTEORPHLLTAHRSADRGTKLLTYLADVYVKNPGRVPR 481
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 508 KDVAAPIDKLPNIKDLPLPGSRDLKQLGPAFARDLREODALAVYDITTFRAHOSLLA 567
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 482 -ELVDPLTKLPTASAGEPPAGSQLLAELGEPGFAKLRESSTIGVTDITFRAHOSLLA 540
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 568 TVRSEFALKPAEAFAVAKLTPELLSVSAWGATYDVAMRFLFEDPDWRDLDELREAMPVNI 627
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 TVRVTKDLAVAPVAVARTLPQLLSLECGWGGATYDVALREFLAEDPWERLAALREAVPNLCL 600
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 628 QMLLRGNVTGYTPYDPSVCRFAKRAASGVDFIRFDALNDVYSQMRPAIDAVLENTA 687
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 QMLLRGNVTGYTPYTPETDAFVQEAATGIDIFRFDALNDVYEQMRPAIEAVRQTGSA 660
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 688 VAEVAMASGDLSDPNEKLYTLDYLMKMAEIVKSGAHILAIDMAGLLRPAAVTKLVTA 747
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 VAEVALCYFADLSDPSELYTLDYLLAEQIVNAGAHVLAVKDMAGLLRPAATAILVSA 720
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 748 LRREFDLPVHVHTHTAGGQATATYFAAAGADAVDAGASAPLSTGTSQPSLSAIVAAFAH 807
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 721 LRREFDLPVHLHTHTGGGLATYLAIAQADAVDAGASAPLSTGTSQPSLSAIVAAFAH 780
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 808 TRDPTGLSLEAVSDLEPYWEAVRGLVLPESGTPGTGRVYRHEIFGGQSLNLRQATAL 867
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 781 TERPTGLDQAVGDLPEPYWESVRKVYAPFAGLASPTGRVYRHEIFGGQSLNLRQATAL 840
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 868 GLADRFELIEDNVAAYNEMLRGPTKVTTPSKVVGDLALHLVAGVDPADFAADPKQYDIP 927
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 841 GLGDRFEDIEAMTAADRMGLRLVKKVTPSKVVGDLALHLVAGVSPADEQDPDFDIP 900
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 928 DSVIAFLRGLGNPPGGWPEPLRTRALEGRSEKAPLTVPEEQAHLDAADDKERNNSL 987
    ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DR	EMBL; AF509529; AAM92771.1; -
DR	InterPro; IPR005482; Biotin_carb_C.
DR	InterPro; IPR000089; Biotin_lipoyl.
DR	InterPro; IPR005479; CPase_LD2.
DR	InterPro; IPR005481; CPase_LN.
DR	InterPro; IPR000891; CPase-Like.
DR	InterPro; IPR003379; PYC_OADA.
DR	InterPro; IPR005930; Pyruv_carbox.
DR	Pfam; PF02785; Biotin_carb_C; 1.
DR	Pfam; PF00364; Biotin_lipoyl; 1.
DR	Pfam; PF02889; CPSase_Lchain; 1.
DR	Pfam; PF02786; CPSase_LD2; 1.
DR	Pfam; PF00682; HMGL-like; 1.
DR	Pfam; TIGR0436; PYC_OADA; 1.
KW	TIGRFAMS; TIGR01235; pyrUV_carbox; 1.
KW	Ligase.
SQ	SEQUENCE 1178 AA; 127253 MW; F0722FEAB8BF39A5 CRC64;
	Query Match. 43.5%; Score 2550.5; DB 13; Length 1178;
	Best Local Similarity 47.5%; Pred.No. 7.6e-128;
	Matches 559; Conservative 168; Mismatches 416; Indels 33; Gaps 15;
QY	7 GLLLLKGIIIV-----SPTTSSTLPFAFKKILVANGETAVRAFRALLETGAATVAIY 59
Dd	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd	9 GGRRALLGAWRLPLPPPGSVRSASQP-IRKVIVANNGEIAIRFRACTELGTURVAVY 67
QY	60 PREDRGFSHRSFASEAYRIETGESPVRYAKYLIDIELTIGAARKVKADAIYPGYGFLSEN AOL 119
Dd	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd	68 SEQDTGMHQRKADEAYLVGRGLFPVQAYLHVPIIRVARENAVDAIHFGYGFLSERADF 127
QY	120 ARECAENGITFIGTTPVELDLTGDKSRAVTAACKAGLPVL-AESTPSKNIDDIVKSARGO 178
Dd	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd	128 AQACVDAGVFVGVPPEVRVMGDKEARSTAAAGVPVPVPGTSAPVATLTGEAQDFAARV 187
QY	179 TYPIFYKAVAGGGGRMFRVSSPDELKKLAYEASREAEAAFGDSGVYVERAVINPQHLEV 238
Dd	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd	188 GFPIIFKAHHGGGGRMAVRVGPQLLEESFSRASSELAARAGDGALFVEKLWERPHHEG 247
QY	239 QILGDRTEGVVHLERYDCSLQRRHQKVVEIAPAQHLDPEDLRDICADAKVKFCRSIGOGA 298
Dd	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd	248 QILGDXHGNNVHLERYDCSIQRRHKQVVIEIAPAARDLPQLRAQLASDAVRIAQQVG YEN A 307
QY	299 GTVEFLVDEKGNHVFIEMNPRIQVEHTVTEVDLVKAOMRIAAGAATLKELGTQDKI 358
Dd	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd	308 GTVEFLVDRDGHKFIEVNSRLQVEHTVTESIITGVLDLVQAQLLVAAGRSLSLGELGQDSV 367
QY	359 KTHGALQCRTTTEDPNNGRPFDGTTITAYSPSGAGVRLDGOAQL-CGETAHFSDMLV 417
Dd	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd	368 RVNCALQCRVTTTEDPARGFQPDTRGLEVFNRMSGMGIRLDGSAFOGALISPHYDSLIV 427
QY	418 KMTCRGSDFFETAVARAORALAEFTVSGVATTNIIGFLRALLRLEEDETSKRIATGFGTDHPHL 477
Dd	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd	428 KVIAHGPDQPSAAKMSRALGEFRIRGVKTNIPLQNVLVAPHQFLGGADVTFQIDENPEL 487
QY	478 LQAPPADDEGRILDYLDVTNVKPCHGVRP-KDVAAPIDKLPNTIKDLPLPGGS-----RD 531
Dd	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd	488 FHLPSONRAQKLHYLGHVMVNGPSTPLPKAKAAVVPEPYPP----PVPMPGPSPEGLRA 543
QY	532 RLKOLGPAATARDLREQDALAVTOTTFDAHQSLLATVRVSFALKPAEAENVAKLTPELLS 591
Dd	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd	544 VLOREGPAGFARALRHGRHLLXLLXTTTFDAHQSLLATVRTRDLARIAPFAVHAHSLSPLCS 603
QY	592 VEAMGGATDYVAMPRLFEPDWRLDELREAMPNVNIOMLLRGNTVGVTPYPDSCVCFAPV 651
Dd	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd	604 METWGGAFTVAMREFLHCPEWRERELRRLVPNIPFMILLRGANAAGVINTPNDVIYRFC 663
QY	652 KEAASSGVDIRIFDALNDVSCMRPAIDAVLETNTAVAEVAMAYSGDLSDPNEKIYTLDDY 711
Dd	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd	664 EVAANGMDIRIFDALNYLNLGIVEAVGRAG-AVVEAALSYTGDVADPTRTKYSLDY 722
QY	712 YLMMAEEIVKSGAHILA TKOMAGLLRPAAVTKLYALTALREF-DLPVWHHTHTTAGGQLAT 770
Dd	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd	723 YLGIKALELVAGTHTLICDKMAGLITPAAAARLLVSSLRDDRPDPVPIHVHTHTDACAATA 782

QY	771	YFAAAGADAVD	GASAPLSGTTGTSQPSLSAIVAAFAHTRDRTGLSLVAVSDLEPYWEAVR	830		
Db	783	LLAAANADADV	DVAVDAMSGMTSQPSMGALVACARGTPLDTGIALSRVFEYSEYEWGAR	842		
QY	831	GLXLPESGTPG	TGR--VYRHETPGCOLSNIRAQATGALGADREFELLIEDNYAAVNEMLG	888		
Db	843	GLVAAFDCTAT	MSGNADVNETIPGGQYTNLHFQAHMGLGHKFEVKKAYAEANKLLG	902		
QY	889	RPTKVTPTSS	KVVGDGLALHLVAGVDFADFPQKYDIPDSVIAFLRGELSGNPPGWPPEP	948		
Db	903	DLIKVTPTSS	KVVGDGLAQCFMVQNGLSRDEAEARADELSFPLSVVEFLOGYIGTPPGGPEP	962		
QY	949	LRTRALEG--	RSRGKAPLTVPEEQQA--HLDADDS--KERNNSLNRLLFPPPTTEFLE	1001		
Db	963	FRSKVLKDL	FRVGRPGASLPPLDFAELSGELGARDGTPSPEDLLSAALYPKVYAEFRD	1022		
QY	1002	HRRRFGNTS	ALDDREFPYGLVEGRETLIRLPDVRTPLLVRLDAISEPDDKGMNVVANVN	1061		
Db	1023	FTSTFGPV	SLGTLFLFEGFTIAEEFEVELEKGT-LHIKALALGDLNAAGQREAFELN	1081		
QY	1062	GOIRPMRVR	DRORSVESVTATAEKADSSNKGHVAAPFAG-VYTVTVAEGDEVKAGDAVAIIE	1120		
Db	1082	GQLRSILVR	DTQALKEMHVHPKADRSAGQGVGAPMPGEVVEVRKVEGEAVEKGAPLCVLS	1141		
QY	1121	AMKKEATIT	ASVDGKTIERVVVPRAKTVKSGDLIVVV	1156		
Db	1142	AMKMETVT	VPAPRGTVSRHLHVRFGMSLEGDDLIAEI	1177		
RESULT 10						
QY	Q9K9M0					
ID	Q9K9M0	PRELIMINARY;	PRT;	1150 AA.		
AC	Q9K9M0;					
DT	01-OCT-2000	(TrEMBLrel. 15, Created)				
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)				
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)				
DE	Pyruvate carboxylase.					
GN	PYCA OR BH2625.					
OS	Bacillus halodurans.					
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.					
OX	NCBI_TaxID=86665;					
RP	[1]					
RN	SEQUENCE FROM N.A.					
RC	STRAIN=C-125 / JCM 9153.					
RX	MEDLINE=20512562; PubMed=11058132;					
RA	Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,					
RA	Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,					
RA	Horikoshi K.;					
RT	"Complete genome sequence of the alkaliphilic bacterium Bacillus					
RT	halodurans and genomic sequence comparison with Bacillus subtilis."					
RL	Nucleic Acids Res. 28:4317-4331(2000).					
DR	EMBL;	AP001516;	BAB06344.1;	-.		
DR	HSP;	P24182;	IBNC.			
DR	InterPro;	IPR005482;	Biotin_carb_C.			
DR	InterPro;	IPR000089;	Biotin_lipoyl.			
DR	InterPro;	IPR005479;	CPase_L_D2.			
DR	InterPro;	IPR005481;	CPase_L_N.			
DR	InterPro;	IPR000891;	HMGL-like.			
DR	InterPro;	IPR003379;	PYC_OADA.			
DR	InterPro;	IPR005930;	Pyruv_carbox.			
DR	Pfam;	PF02785;	Biotin_carb_C.1.			
DR	Pfam;	PF00364;	Biotin_lipoyl.1.			
DR	Pfam;	PF00289;	CPSase_L_chain.1.			
DR	Pfam;	PF02786;	CPSase_L_D2.1.			
DR	Pfam;	PF00682;	HMGL-like.1.			
DR	Pfam;	PF02436;	PYC_OADA.1.			
DR	TIGRFAMS;	TIGR01235;	Pyruv_carbox.1.			
DR	PROSITE;	PS00867;	CPSASE_2.1.			
KW	Complete proteome.					
SQ	SEQUENCE	1150 AA;	128858 MW;	ED6708B9A9F3BD4 CRC64;		

Best Local Similarity 46.9%; Pred. No. 4.6e-127; Matches 540; Conservative 185; Mismatches 399; Indels 27; Gaps 13;	
QY 26 LPFAFKILVANGETAVRAFAAETGAATVAIYIPREDGRSGHRFASAVRIGTIGSV 85	
Db 4 LKNIKVLVANGETAIVRAFAAETGAATVAIYIPREDGRSGHRFASAVRIGTIGSV 85	
QY 86 KAYLOIDEIGAAGKADAIYPGYGFLENQAOLARECAENGITFTGPTPEVLDLTDGKS 145	
Db 64 EAYLDIEGIIETAKRHGVDAIHGPGYGFLENQAOLARECAENGITFTGPTPEVLDLTDGKS 145	
QY 146 RAVTAAKAGLVLAEST-PSKNIDDIYKSAQGYPIPVKAVAGGSGMRFSVSPDL 204	
Db 124 QAREQAIKANLVIPGSDGVSLVEDVAFADKHGYPFIKAALGGGGRGMRVSEN 183	
QY 205 RLKATEASREARAAGDGVYVERAVINPOHTVEOILGDRTEVHLVYDCSLORRHK 264	
Db 184 QSYERAKSEAKAAGNDVEYVEKTEIENPKHIEVOILADKHGTHLHLYDCSVORRHK 243	
QY 265 VVEIAQAHLDELDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFIEINPQIYVSH 324	
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QY 325 TVTEEVTEVDIYKAOHRLAAGTL--KEGL--TQDKITHGAALOCRTTDPNNGFRD 381	
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QY 382 TGTITAYSPGGAGVRLD--GAOLGGETTAHFDLSMLVMTCRGSDFFATAVARAQAALAEF 440	
Db 364 TGRINAYRSGGFGVRLDAGNGFQAVITPYDLSLVKSTWALTFEGAAKMLNREF 423	
QY 441 TVSGVATNIGFRLALREDEFTSKRIATGFIGDHPHLLQAPPADDEOGRILDYADVTVN 500	
Db 424 RIRGIKTIAFLENVQHQFSLGSEYNTSFIDOTPELFVFKKRGKMLSFICETIVN 483	
QY 501 KPHGVPRDXVAAPIDK--LPNIK-DLPLPGSRDRILKQLGPAAPARDIREQDALAVTDT 557	
Db 484 GYPLGE-KTKPVDPKVPKLVKLEPIDGDKQILDGHPGSLAKWKEQKHVLLTDT 542	
QY 558 FRAHQSLATVRSFALKPAAEVAKLTPELLVSEAMGGATYDVAMRFLDPDWRLDE 617	
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QY 618 LREAMPNNVQMLGRNTVGYTPDPSVCRAPVKEAASSGVDPIDRFDALNDVSMRPA 677	
Db 603 LRKAPNVLFOMLLASNAVGYKNYPDNLIRFVDKSNAGIDVFRIDSLNWNVEGMKLA 662	
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QY 858 SNLRQAATAGLIADRFELIEDNYAAVNEMLGRPTKVTPTSSKVVGDALHLVAGVDPAF 917	
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QY 918 AADPKYDIPDSVIAFLRGEIGNPGGWPPELRLTRALEGRSEGKAPLVEVPEEQAHLDA 977	
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QY 1027 TLIRLPDVRTPLVRLDAISEPDDKGMNRNVANVGQIRPMVRDRSVESVTATAEKADS 1086	

Db 1018 IEVEIPQKKT-LIVKFSLSKQDDGNRIYVPELNGQPREVLKQDSVKTISIISREKADK 1076	
QY 1087 SKGHVAAFPAG-VYTVTVAGDEVKAGDAVAIIIEAMKEATITASVDGKIRVVVPAAT 1145	
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QY 1146 KVEGGDLIVV 1156	
Db 1137 AIQTGDLLIEV 1147	

RESULT 11
Q9KWU4
ID Q9KWU4 PRELIMINARY; PRT; 1148 AA.
AC Q9KWU4;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1).
GN PYCA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fricz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Guay B.J., Goffeau A., Gollightly E.J., Grandi G., Guseppi I., Guy P.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinis S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.J., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Taccioni E., Takagi T., Takahashi H., Takenaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zmstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
RL Nature 390:249-256(1997).
RN [2]
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z99111; CAB13359.1; -;
DR HSSP; P24182; 1BNC.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; Ccase_L_D2.
DR InterPro; IPR005481; Ccase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
PFam; PF02785; Biotin_carb_C; 1.


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Db 327 YFTEINPRQVEHTVTEEDVLAQOMRLAAGATLKGELGLTQDKTKTHGAALQCRIT 386
QY 372 EDNNGFRPDGTITAYRSPGGAGVRLDGAQAQGGF-ITAFHDSMLVKMTCRSGSDPETAV 430
Db 387 EDPKSGFSDPTGKIEYRSGAGVRLDGGNGFAGALITPHYDSMLVKMTCRSGSTYIAR 446
QY 431 ARAQALAEFTVSGVATNIGFLRALIREEDFTSKRTATGFIGDHPHLLQAAPPDQGR 490
Db 447 RKVVALVEFRIGVATNIPFTSLSHPVFVDGTCTWTFIDTPELFAVLSQNRQAQL 506
QY 491 LDYLDADVTYN---KPHGVRPK---DVAAPI---DKLPNIKDLPLP---RGSRRDLKQLGPA 539
Db 507 LAYLGDVAVNGSSIKQIGEPKLGDIIRKPLVHDAAGKPLDVSVPATKWKQKILDSEGE 566
QY 540 AFARDLREQDALAVTDTTFRDAHQSLLATVRFSFALKPAAEAVALKUTPELLSVEAWGAT 599
Db 567 AFARAVRANKGCLIMDTWRDAHQSLLATVRFTIDLLNAHETSHALANAYSLECWGAT 626
QY 600 YDAMRFLFEDPWDRDELREAMPNVNIOMLLRGRNTVGYTPYDPSVCRFAVKEARSSGV 659
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QY 660 DIFRIFDALNDVQSMPAIDAVLENTAVAEAMAYSGLDSPNEKLYLTDLYLKMAEEL 719
Db 687 DIFRVPDALNDVDQEVGKAV-HAAEGVVEATICYSGDMLNPSKK-YNLPYVLDLVDKV 744
QY 720 VKSGAHLAKMAGLLRPAATKLVLTALRRFF-DLPVHVHTHDAGGOLAYFYAAQAQ 778
Db 745 VOFKPHVLGDKMAGVYKQARLLGSTRERYPDLPVHVHTHDSAGTGVASMIACAQAG 804
QY 779 ADADGASAPLGGTTSQPSLSAIVAAFAHTRDRTGLSLEAVSDLEPYWEAVRGLYLPES 838
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QY 839 GTPGPTGRVYRHEIPGGQSLNRAQATALGLADREFELIEDNYAAVNEMLRGPTKVTTPSSK 898
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QY 899 VVGDLALHLVAGVDPADFAAPDKYDIPDSVIAFLRGLNPPGWPPEPLTRALEGRS 958
Db 925 VVGDLAQFMVSNKLTAEADVIAKAGELDFPGVLEFLGLMQPGYGGFPPEPLSRALDRR 984
QY 959 E-GKAP-----LTEVPEEQAHLDADDKERRNSLNRLFPKPTPEEFLEHRRR 1005
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QY 1006 FGNTSALDDREFYGLVSGREFLIRLPDVRTPLLVRLDAISE-PDDKGMNRNVANVNGOT 1064
Db 1038 FGDSLPLTRYFLAKPEIGEEHFEVELEKGV-LILKLLAIGLPSLSEQTQGREVFYVNGEV 1096
QY 1065 RGMVRDRSVESVTAAEKSSNKGHVAAPAGVVT-VTVAGDEVKAGDAVAITEAMK 1123
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Db 1157 MEMWISAPHSKGVSSLLYKESGSDVGDQLV 1186

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RESULT 15

Q8Y846

ID

Q8Y846

AC

Q8Y846

DT

01-MAR-2002

(reMBLrel. 20, Created)

DT

01-MAR-2002

(reMBLrel. 20, Last sequence update)

DT

01-MAR-2003

(reMBLrel. 23, Last annotation update)

DE

PycA protein.

PYCA OR LM01072.

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OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacilliales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian L.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Ndjari H.,
RA Nordisiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591977; CAC99150.1; -.
DR ListList; LM001072; -.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF02786; CPase_L_chain; 1.
DR Pfam; PF02786; CPase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRfams; TIGR01235; pyruv_carbox; 1.
DR PROSITE; PS00866; CPASE_1; 1.
DR PROSITE; PS00867; CPASE_2; 1.
DR Complete proteome.
KW SEQUENCE 1146 AA; 128049 MW; A062F8C9A092B6F CRC64;

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Query Match 42.5%; Score 2494; DB 16; Length 1146;
Best Local Similarity 45.7%; Pred. No. 7.7e-125;
Matches 525; Conservative 186; Mismatches 408; Indels 30; Gaps 11;

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Db 5 KKLIVANRGEIARVNRACTELKIKITVAIYSQEDTSGFHRYSKSDAAYLVGAGKKPIDAYL 64
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Db 65 DIENIETAKESGADAIHPGYGFLSENIEFARRCQEGIFVGPYKSKHDMFGDKIKAKE 124
QY 150 AAKKAGLPVLAEST-PSKNIDDIVKSAEGOTPIFVKAVAGGGGRMRPVSSPDDELKLA 208
Db 125 QALLADIPVPGSNPGVAGIKEVEFEGKNGPIPMKASLGSGGGRMRVSEKHEVKESF 184
QY 209 TPASREAEAAFGDGVYVERAVINPQIHIEVQILGDRTEGVHLYPRDCSLORRHOKVBI 268
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QY 269 APAQHLDELDRICADAVKFCRSIGYQAGCTVEFLVEKGNHVIEMNPRIQVEHTVTE 328
Db 245 AFENAITSELNRNRCIDAAVKLMKNVDYINAGVFEELV-EGDDFYFIEVNPVQVEHTITE 303
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Db 304 MITGIDIVQSQFLFIADGVALHDLQVLAIPKQEDIIHIGSAIQSRITTEPLNNFMDPTGRV 363
QY 386 TAYRSPGGAGVRLD-GAAQLGGEITAFHDSMLVKMTCRSGSDPETAVARAQALAEFTVSG 444
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 424 VTNIPFLNVRHDPFAGSNNTSFDITTPFLFEPHTRDRGKTLRYIGNVYNGFFG 483
 QY 505 VRPKOVAAPIDKLPNIKDLF-----LFRGSRDRLKQLGPAFAFARDLREQDALAVTDTFRD 560
 Db :
 484 IKHRD--KPYAEPRLPKIPYGSQISPGTKQILDAGKPEGVVDWVKQKEVLLTDTLRD 541
 QY 561 AHOSLLATVRFAKPAEAFAKLPPELLSVBEGGAYDVAMRFLFEDPDWRDLDELRE 620
 Db :
 542 AHOSLLATVRSKDIFQVADAMAHLPLPNMFSEFMGGATFDVAYRFLNEDPWVRLTLRK 601
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 Db : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
 602 QIPNVFMQMLLGGANAVGKNPDNVIREFVKSQSGVDVFRVFDLSLWIKMEVMSIDA 661
 QY 681 VLENTNVAEAMAYSGDLSDPNEKLYTLDYILKMAEIVKSGAHILAIKDMAGLILRPAA 740
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 901 GTIDFPDSVIEFFMGEICQPTGGPEKQKLVKQRT----PLDRPGALMEPVNFVDY 956
 QY 981 K-----ERRNSLNRLLFPKPTBEEFLEHRRFRFGNTSALDDREFFYGLVEGRETLI 1029
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 QY 1030 RLPDYVETPLILRLDAISEPDDKGMNVVANVNGQIRPMVRDRSVESVTATAEKADSSNK 1089
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 1136 SCDLLIEVN 1144

Search completed: September 24, 2003, 15:59:11
 Job time : 95.6387 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 24, 2003, 15:51:28 ; Search time 88.3413 seconds
(without alignments)
3330.038 Million cell updates/sec

Title: US-09-974-973a-19

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Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23.*

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mnc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.rodent.*
- 12: sp.virus.*
- 13: sp.vertibrate.*
- 14: sp.unclassified.*
- 15: sp.rvirus.*
- 16: sp.bacteriap.*
- 17: sp.archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	5788	100.0	1140	16	O54587
2	5759	99.5	1140	2	Q8L2G4
3	5317.5	91.9	1168	16	Q8FRO0
4	5305.5	91.7	1139	2	Q8QRL2
5	3799	65.6	1124	16	Q9RK64
6	3783.5	65.4	1127	2	Q9F843
7	3712.5	64.1	1127	16	P95127
8	3483	60.2	1124	2	Q50450
9	2552	44.1	1178	13	Q8JHF6
10	2525.5	43.6	1150	16	Q9K9M0
11	2524	43.6	1148	16	Q9K9M0
12	2519.5	43.5	1180	13	Q9DDT1
13	2509.5	43.4	1192	3	Q9HES8
14	2505	43.3	1147	2	P94448
15	2493	43.1	1146	16	Q9Y846
16	2491.5	43.0	1144	16	Q97FR7

SUMMARIES

ALIGNMENTS

RESULT 1

O54587 PRELIMINARY; PRT; 1140 AA.
 ID O54587
 AC O54587;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Pyruvate carboxylase (EC 6.4.1.1).
 GN PYC OR CGL0689.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=21253;
 RA Koffas M.A.G., Ramamoorthi R., Pine W.A., Sinskey A.J.,
 RA Stephanopoulos G.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032;
 RA Peters-Wendisch P.G., Kreutzer C., Kalinowski J., Patek M., Sahn H.,
 RA Bismanns B.J.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RL "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
 RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- COFACTOR: BIOTIN (BY SIMILARITY).
 DR EMBL; AF038548; AAB92588.1; -;
 DR EMBL; Y09548; CAA70739.1; -;
 DR EMBL; AP005276; BAB98082.1; -;
 DR HSP; P24182; LBNC.
 DR InterPro; IPR001882; Biotin_attach.
 DR InterPro; IPR005482; Biotin_carb_C.
 DR InterPro; IPR000089; Biotin_lipoyl.

Q92CW1 listeria in
 Q8nx69 staphylococ
 Q9uy8 staphylococ
 Q93918 aspergillus
 Q8fy0 brucella su
 Q8ubx3 agrobacteri
 Q98f27 rhizobium i
 Q8y120 brucella me
 Q8cpm3 staphylococ
 Q17732 caenorhabdi
 Q8ayn3 pagrus majo
 Q9ueel schizosacch
 Q9xz00 drosophila
 Q8xt03 pichia angu
 Q92113 rhizobium m
 P78822 schizosacch
 Q8mkw5 drosophila
 Q16921 aedes aegypt
 Q8er83 oceanobacil
 Q9chg7 lactococcus
 Q9rat6 lactococcus
 Q59740 rhizobium e
 Q8axq6 pagrus majo
 Q9xdj1 bacillus ce
 Q62043 mus musculu
 Q9kwu5 bacillus su
 Q8bp54 mus musculu
 Q8mkw4 drosophila
 Q8mkw3 drosophila

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DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF02786; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01235; pyruv_carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
KW Biotin; Ligase; Pyruvate; Complete proteome.
SQ SEQUENCE 1140 AA; 123102 MW; 2A6D4B4ED2FEB531 CRC64;

Query Match          100.0%; Score 5788; DB 16; Length 1140;
Best Local Similarity 100.0%; Pred. No. 1.9e-302;
Matches 1140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTHTSSTLPAPKFKILVANRGEIAVRAFAALETGAATVAIYPREDRGSFHRSEAVR 60
Db 1 MSTHTSSTLPAPKFKILVANRGEIAVRAFAALETGAATVAIYPREDRGSFHRSEAVR 60

QY 61 IGTEGSPKAYLIDIDEITGAKKVKADAIYPGYGFLSNAQLARECAENGTFIGTPEV 120
Db 61 IGTEGSPKAYLIDIDEITGAKKVKADAIYPGYGFLSNAQLARECAENGTFIGTPEV 120

QY 121 LDLTGDKSRVTAANKAGLPVLAESTPSKNIDEIVKSAEGQYIPFVKAVAGGGRGMRF 180
Db 121 LDLTGDKSRVTAANKAGLPVLAESTPSKNIDEIVKSAEGQYIPFVKAVAGGGRGMRF 180

QY 181 VASPDILAKLATEASREAEAFGDAVYVRAVINPQHIEVOILGDHTGEVVLHYERDCS 240
Db 181 VASPDILAKLATEASREAEAFGDAVYVRAVINPQHIEVOILGDHTGEVVLHYERDCS 240

QY 241 LQRRHQKVEIAPAOHLPELDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEWN 300
Db 241 LQRRHQKVEIAPAOHLPELDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEWN 300

QY 301 PRIQVEHTVTEVTEVDLVKQMRLAAGATKELGLTQDKIKTHGAALQCRITTEDPNNG 360
Db 301 PRIQVEHTVTEVTEVDLVKQMRLAAGATKELGLTQDKIKTHGAALQCRITTEDPNNG 360

QY 361 PRPDTGTTAYRSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFFETAVARAQAL 420
Db 361 PRPDTGTTAYRSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFFETAVARAQAL 420

QY 421 ABFTVSGVATNIGFURALLREEDFTSKRTATGFIADHPHLLQAPPADDEQGRILDYLDV 480
Db 421 ABFTVSGVATNIGFURALLREEDFTSKRTATGFIADHPHLLQAPPADDEQGRILDYLDV 480

QY 481 TVNKPFGVPRKDVAAIPDKLPNIKDLPLPRGSRDLKQIGPAAFAARDLREQDALAVTDT 540
Db 481 TVNKPFGVPRKDVAAIPDKLPNIKDLPLPRGSRDLKQIGPAAFAARDLREQDALAVTDT 540

QY 541 FEDAQSLLATVRSFALKPAAEAVALKTELLSVEANGGATYDYAMRFLFEDPDWRDLDE 600
Db 541 FEDAQSLLATVRSFALKPAAEAVALKTELLSVEANGGATYDYAMRFLFEDPDWRDLDE 600

QY 601 LREAMPNVIOMLLGRNTGVTPYPSDVCRAVKEAASSGVVDIFRIFDALNDVSMRPA 660
Db 601 LREAMPNVIOMLLGRNTGVTPYPSDVCRAVKEAASSGVVDIFRIFDALNDVSMRPA 660

QY 661 IDAVLETNTAFAEAMAYSGDLSDPNEKLYTLDDYLYLKMAEEIVKSGAHILAIDKMWGLLR 720
Db 661 IDAVLETNTAFAEAMAYSGDLSDPNEKLYTLDDYLYLKMAEEIVKSGAHILAIDKMWGLLR 720

QY 721 PAAVTKLVTALREFDLPHVHTHTDTAGQLATYFAAQAQADADVDGASAPLSGTTSQPS 780
Db 721 PAAVTKLVTALREFDLPHVHTHTDTAGQLATYFAAQAQADADVDGASAPLSGTTSQPS 780

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QY 781 LSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 840
Db 781 LSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 840

QY 841 SNLRAQATALGLADRFELIEDNYAANEMLRPTKVTPTSSKVVGDIALHLVAGVDPADF 900
Db 841 SNLRAQATALGLADRFELIEDNYAANEMLRPTKVTPTSSKVVGDIALHLVAGVDPADF 900

QY 901 AADPOKYDIPDSVIAFLRGLGNPPGGWPEPLRTRALEGRSGKAPLIEVPEEQAHLLDA 960
Db 901 AADPOKYDIPDSVIAFLRGLGNPPGGWPEPLRTRALEGRSGKAPLIEVPEEQAHLLDA 960

QY 961 DSKERRNSLNRLLPKPTPEEFLEHRRRFGNPTSAIDREFFYGLVGEVRETLLRLPDVRIP 1020
Db 961 DSKERRNSLNRLLPKPTPEEFLEHRRRFGNPTSAIDREFFYGLVGEVRETLLRLPDVRIP 1020

QY 1021 LLVRDLDAIASEPDDKGMNVVANVNGQIRPMRVDRSVESVTATAEKADSSNKGHVAAPFA 1080
Db 1021 LLVRDLDAIASEPDDKGMNVVANVNGQIRPMRVDRSVESVTATAEKADSSNKGHVAAPFA 1080

QY 1081 GVVTVTVTAEGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVYVPAATKVEGGDLIVVVS 1140
Db 1081 GVVTVTVTAEGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVYVPAATKVEGGDLIVVVS 1140

RESULT 2
Q8L2G4
ID Q8L2G4 PRELIMINARY; PRT; 1140 AA.
AC Q8L2G4;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Pyruvate carboxylase.
GN PYC.
OS Corynebacterium crenatum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=168810;
RW [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD945;
RA Wang J., Ding J., Liu Y.;
RT "Cloning and Expression of Pyruvate Carboxylase Gene in
RT Corynebacterium crenatum CD945.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF503915; AAM27458.1; -.
DR InterPro; IPR001882; Biotin_attach.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_L_D2.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01235; pyruv_carbox; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00867; CPSASE_2; 1.
SQ SEQUENCE 1140 AA; 123126 MW; FFA90BB7644C910E CRC64;

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Query Match          99.5%; Score 5759; DB 2; Length 1140;
Best Local Similarity 99.3%; Pred. No. 6.9e-301;
Matches 1132; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSTHTSSTLPAPKFKILVANRGEIAVRAFAALETGAATVAIYPREDRGSFHRSEAVR 60
Db 1 MSTHTSSTLPAPKFKILVANRGEIAVRAFAALETGAATVAIYPREDRGSFHRSEAVR 60

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QY 61 IGTGSPVKAYLIDIDEIIIGAAKKVKADAIYPGYFLSENAQLARECAENGITFIGPTPEV 120
Db 61 IGTGSPVKAYLIDIDEIIIGAAKKVKADAIYPGYFLSENAQLARECAENGITFIGPTPEV 120
QY 121 LDLTGDKSAVTAANKAGLPVLAESTPSKNIDEIVKSAEGQYPIPVKAVAGGGGRMF 180
Db 121 LDLTGDKSAVTAANKAGLPVLAESTPSKNIDEIVKSAEGQYPIPVKAVAGGGGRMF 180
QY 181 VASPELRLKATEASREAAFGDGAIVYVERAVINPOHLEVOQLGDHTGEVHLYERDCS 240
Db 181 VASPELRLKATEASREAAFGDGAIVYVERAVINPOHLEVOQLGDHTGEVHLYERDCS 240
QY 241 LQRRHQKVVEIAPAQHLDELDRICADAVKFCRSIGYQAGTVEPLVDEKGNHVFIEMN 300
Db 241 LQRRHQKVVEIAPAQHLDELDRICADAVKFCRSIGYQAGTVEPLVDEKGNHVFIEMN 300
QY 301 PRIQVEHTVTEVEVDLVKQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNNG 360
Db 301 PRIQVEHTVTEVEVDLVKQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNNG 360
QY 361 FRPDTGTITAYRSPGGAGVRLDGAOLGGEITAHFDSMLVKMTCRGSDFTAVARAQAL 420
Db 361 FRPDTGTITAYRSPGGAGVRLDGAOLGGEITAHFDSMLVKMTCRGSDFTAVARAQAL 420
QY 421 AEFTVSGVATNIGFLRALLREDEFTSKRIATGFIADPHPLLQAPPADDDQGRILDYADV 480
Db 421 AEFTVSGVATNIGFLRALLREDEFTSKRIATGFIADPHPLLQAPPADDDQGRILDYADV 480
QY 481 TVNKHGVPKQVAAPIDKLPNIKOLPLPRGSRDLKQLGPAAFARDLREQDALAVTDIT 540
Db 481 TVNKHGVPKQVAAPIDKLPNIKOLPLPRGSRDLKQLGPAAFARDLREQDALAVTDIT 540
QY 541 FRDAHOSLLATVRSPFALKPAEAVAKLPPELLSVEAWGGATVDVAMRFLFEDPWDRLE 600
Db 541 FRDAHOSLLATVRSPFALKPAEAVAKLPPELLSVEAWGGATVDVAMRFLFEDPWDRLE 600
QY 601 LREAMPNVNIQMLLRGNTVGTPTPDSVCRAFPKAASSGVDIFRIFDALNDVSQMRPA 660
Db 601 LREAMPNVNIQMLLRGNTVGTPTPDSVCRAFPKAASSGVDIFRIFDALNDVSQMRPA 660
QY 661 IDAVLETNITAVAFVAMAYSGDSDPNEKLYLDYILKMAEIVKSAHILAIKDMAGLLR 720
Db 661 IDAVLETNITAVAFVAMAYSGDSDPNEKLYLDYILKMAEIVKSAHILAIKDMAGLLR 720
QY 721 PAAVTKLVTALRREFDLPVHVHTDITAGGOLATYFAAAQAGADAVDGASAPLSGTTSQPS 780
Db 721 PAAVTKLVTALRREFDLPVHVHTDITAGGOLATYFAAAQAGADAVDGASAPLSGTTSQPS 780
QY 781 LSAIVAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 840
Db 781 LSAIVAFAHTRRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGGQL 840
QY 841 SNLRAQATAGLADREFLEDNYAANEMLGRPTKVTTPSSKVVDLALHLVAGVDPADF 900
Db 841 SNLRAQATAGLADREFLEDNYAANEMLGRPTKVTTPSSKVVDLALHLVAGVDPADF 900
QY 901 AADPQKYDIPDSVIAFLGELGNPPCGWPEPLTRALEGRSEKAPLTVPEPEQAHILDA 960
Db 901 AADPQKYDIPDSVIAFLGELGNPPCGWPEPLTRALEGRSEKAPLTVPEPEQAHILDA 960
QY 961 DSKERRNSLNRLLPKPTPEELHRRRFGNTSALDDREFFYGLVREGRETLRLPDVTRTP 1020
Db 961 DSKERRNSLNRLLPKPTPEELHRRRFGNTSALDDREFFYGLVREGRETLRLPDVTRTP 1020
QY 1021 LLVRLDAISEPDDKGMNVVANNVNGOIRPMRVDRSVESVATAEAKDSSNKGHVAAPFA 1080
Db 1021 LLVRLDAISEPDDKGMNVVANNVNGOIRPMRVDRSVESVATAEAKDSSNKGHVAAPFA 1080
QY 1081 GVVTVTVAEGDEVKAGDAVAIIIEAMKMEATITASVDGKIDRVVVPAAATKVEGGDLIVVYS 1140
Db 1081 GVVTVTVAEGDEVKAGDAVAIIIEAMKMEATITASVDGKIDRVVVPAAATKVEGGDLIVVYS 1140
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RESULT 3
Q8FRQ0 PRELIMINARY; PRT: 1168 AA.
ID Q8FRQ0;
AC Q8FRQ0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Pyruvate carboxylase (EC 6.4.1.1).
GN PYC OR CE0709.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF005216; BAC17519.1; -.
KW Ligase; Complete proteome.
SQ SEQUENCE 1168 AA; 126245 MW; A5D5A4DD4DF285F8 CRC64;

Query Match 91.9%; Score 5317.5; DB 16; Length 1168;
Best Local Similarity 91.2%; Pred. No. 3.8e-277;
Matches 1038; Conservative 43; Mismatches 56; Indels 1; Gaps 1;

QY 3 TTSTSLPAFKILVANRGEIAVRAFAALETGAATVAIYPREDGRGSHRSFASAVRIG 62
Db 32 TTTPSTLPFAFKILVANRGEIAVRAFAALETGAATVAIYPREDGRGSHRSFASAVRIG 91
QY 63 TEGSPVKAYLIDIDEIIIGAAKKVKADAIYPGYFLSENAQLARECAENGITFIGPTPEVLD 122
Db 92 TEGSPVKAYLIDIDEIIIGAAKKVKADAIYPGYFLSENAQLARECAENGITFIGPTPEVLD 151
QY 123 LTGDKSRATVTAAKKAGLPVLAESTPSKNIDEIVKSAEGQYPIPVKAVAGGGGRMFVA 182
Db 152 LTGDKSKAVSAKKAGLPVLAESTPTDIDEIVKSAEGQYPIPVKAVAGGGGRMFVE 211
QY 183 SPDELKLAATESREAAAFGGGAVYVERAVINPOHIEVOQLGDHTGEVHLYERDCSLQ 242
Db 212 KPDELRELAATESREAAAFGGGAVYVERAVINPOHIEVOQLGDHTGDIHLYERDCSLQ 271
QY 243 RRHKQVVEIAPAQHLDELDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFIEMNPR 302
Db 272 RRHKQVVEIAPAQHLDELDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFIEMNPR 331
QY 303 IQVEHTVTEVEVDLVKQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNNGFR 362
Db 332 IQVEHTVTEVEVDLVKQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNNGFR 391
QY 363 PDTGTTATVRSPGGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFTAVARAQALAE 422
Db 392 PDTGTTATVRSPGGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFTAVARAQALAE 451
QY 423 FTVSGVATNIGFLRALLREDEFTSKRIATGFIADPHPLLQAPPADDDQGRILDYADV 482
Db 452 FNVSGVATNIGFLRALLREDEFTSKRIATGFIADPHPLLQAPPADDDQGRILDYADV 511
QY 483 NKPHGVPRDVAAPIDKLPNIKOLPLPRGSRDLKQLGPAAFARDLREQDALAVTDITPR 542
Db 512 NKPHGERP-ETAPPIEKLPEVENIPLPRGSRDLKQLGPEGFARDLREQDALAVTDITPR 570
QY 543 DAHQSLATVRSPFALKPAEAVAKLPPELLSVEAWGGATVDVAMRFLFEDPWDRLEUR 602
Db 571 DAHQSLATVRSPFALKPAEAVAKLPPELLSVEAWGGATVDVAMRFLFEDPWDRLEUR 630
QY 603 EAMPNVNIQMLLRGNTVGTPTPDSVCRAFPKAASSGVDIFRIFDALNDVSQMRPAID 662
Db 631 EAMPNVNIQMLLRGNTVGTPTPDSVCRAFPKAASSGVDIFRIFDALNDVSQMRPAID 690
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DE Hypothetical 120.4 kDa protein (Pyruvate carboxylase).
 GN PCA OR RV2967C OR MTCY349.20 OR MT3045.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;

[1]

SEQUENCE FROM N.A.

SPRAIN-H37RV;

MEDLINE-98295987; PubMed-9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RN Nature 393:537-544 (1998).

[2]

SEQUENCE FROM N.A.

SPRAIN-CDC 1551 / Oshkosh;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z83018; CAB05410.1; -;
 DR EMBL; AE007125; AAK47371.1; -;
 DR HSSP; P24182; 1BNC.
 DR TIGR; MT3045; -;

DR Tuberculium; RV2967c; -;
 DR InterPro; IPR001882; Biotin_attach.
 DR InterPro; IPR005482; Biotin_carb_C.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR InterPro; IPR005479; Cphase_L_D2.
 DR InterPro; IPR005481; Cphase_L_N.
 DR InterPro; IPR000891; PYC_OADA.
 DR InterPro; IPR003379; PYC_OADA.
 DR InterPro; IPR005930; Pyruv_carbox.
 DR InterPro; IPR000634; S/T_dehydrtse.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF00364; biotin_lipoyl; 1.
 DR Pfam; PF02786; Cphase_L_D2; 1.
 DR Pfam; PF02786; Cphase_L_D2; 1.
 DR Pfam; PF00682; HMGL-like; 1.
 DR Pfam; PF02436; PYC_OADA; 1.
 DR TIGRfams; TIGR01235; pyruv_carbox; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 DR PROSITE; PS00867; CPSASE_2; 1.
 DR PROSITE; PS00165; DEHYDRATASE_SSR_THR; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1127 AA; 120422 MW; 84B0A4CC1A23CD90 CRC64;

Query Match

Best Local Similarity 64.1%; Score 3712.5; DB 16; Length 1127;

Matches 730; Conservative 153; Mismatches 239; Indels 11; Gaps 6;

QY 12 FKKLVANRGEIAVRAALETGAATVATVPREDRGSHFSPASEAVRITGSGSPVK 71

DB 2 FSKVLNARGEIAIRAFRAAYELGVTAVVYPEDRNSQRLKADESQIGDIGHVPHAY 61

QY 72 LDIDEITGAAKVADAIYPGYGLFSENQAARECAENGITFTGPTPEVILDTGDKSRV 131

DB 62 LSVDELVAATARRAGADAIYPGYGLFSENPDLAACAAGISFVGPSEVILELAGNSRAI 121

QY 132 TAAKKAGLPVLAESTPSKNIDEIVKSAEGOTYPIFFKAVAGGGGMRFPVSPDELKLA 191

DB 132 TAAKKAGLPVLAESTPSKNIDEIVKSAEGOTYPIFFKAVAGGGGMRFPVSPDELKLA 191

DB 122 AAAREAGLPVLMSSAPSASVDELLSVAAGMPPELFVKAVAGGGGRMRVGDIAALPEAL 181

QY 192 TEASREAAAFGAGVYVERAVINPOHIEVQIIGDHTGEVHLYERDCSLQRHKQVEI 251

DB 182 EAASREAAAFGAGVYVERAVINPOHIEVQIIGDHTGEVHLYERDCSLQRHKQVEI 241

QY 252 APAQHLDPEDLRICADAVKFCRSIGVQAGAGTVEFLVDEKGNHVFTEMNPRIQVEHTVTE 311

DB 242 APAPHLDALRYKMCVDVAFARHIGYSCAGTVEFLDDEGEYVTEMNPRIQVEHTVTE 301

QY 312 ETEVDLVKAOMRLAAGATLKEGLTQDKTKTHGAALQCRITTEDPNNRPPDTGITAY 371

DB 302 EITDVLVASQLRIAAAGETLEQLGLRQEDIAPIHGAALQCRITTEDPANGRPDTRISAL 361

QY 372 RSPGGAGVRLDGAQOIGGETTAHFDMSLYKMTCRGSDFFETAVARAQALAEFTVSGVATN 431

DB 362 RTAGGAGVRLDGSNIGAEISPYFDSMLVKLCRCGRDLPTAVSRRARATAEFTVSGVATN 421

QY 432 IGFRLALLREEDPFTSKRIATGFTADHPHLQAAPADDEQGRILDYLDYLVNPKPHGVKPK 491

DB 422 IPFLQAVLDDPFRAGRVTTSFIDERPQLLTARASADRGTKILNLFADYTVNPNYSRPS 481

QY 492 DVAAPIDKLPNIKDLPL----PRGSDRLKQLGPAAPARDLREQDIALVDTTFRDAHQ 547

DB 482 TI-YPDKLP---DLDLRAAPPAGSKORLVKLGEGFARWLRESAAVGVDTTFRDAHQ 537

QY 548 LLATRVRSFALKPAAEAVALKLTPELLSVEAGWATYDVAMRFLFEQDPWDLDELREAMPN 607

DB 538 LLATRVTSGLSRVAPYLARTMPQLLSVECGWATYDVAMRFLFEQDPWDLDELREAMPN 597

QY 608 VNTQMLLRGNTVGYTPYDPSCVAFVKEAASGVDFIRIFDALNDVQMRPAIDAVLET 667

DB 598 ICLQMLLRGNTVGYTPYPIEIVSAFQVETATGIDIFRIFDALNNIESMRPAIDAVRET 657

QY 668 NTAVAEVAMAYSGDSDPNKLYTLDYLLKMAEIVKSGAHIIAIDKMAGLLPPAAVTKL 727

DB 658 GSAIAEVAMCYTGDLTDPGEQLYTLDYLLKMAEIVKSGAHIIAIDKMAGLLPPAAVTKL 717

QY 728 VTALRRFEDLPVHVHTHTAGGOLATYFRAAQAGADAVDGCASAPLSTTSQPSLSAIVAA 787

DB 718 VSALRSRFDLPVHLHTHTDTPGGQLASYAAAHAGADAVDGAAPLAGTTSQPSLSAIVAA 777

QY 788 FAHTRDRTGLSLEAVSDLEPYWEAVRGLYLPFFESGTPGPTGRVYRHEIPGGQLSNLRAQA 847

DB 778 AAHTDYDTGLSLSAVCALEPYWEALRKVYAPFESGLPGPTGRVYHHEIPGGQLSNLRAQA 837

QY 848 TALGLADRFELIEDNAAVNMELGRPTKVTTPSSKVVGDIALHLVAGVDPAADPADEPKY 907

DB 838 IALGLGDFEIEEAYAGADRVILGRVKTPTTKVYVGDIALHLVAGVDPAADPADEPKY 897

QY 908 DIPDSVIAFLRGELGNPPPGGWPPELRTALRESEKGLPELTPVEPEEQAHLDDADDGKERR 967

DB 898 GIPESVILGFLRGELGNPPPGGWPPELRTALRESEKGLPELTPVEPEEQAHLDDADDGKERR 955

QY 968 NSLNRLFFPKPTEEFLEHRRRFGNTSALDDREFFYGLVGEHREFTLIRLPDVRTPLVRLDA 1027

DB 956 ATNRLRLFTSPTKEFNEHREAYGDTLSQSANQFFYGLRQGEHVRKL-ERGVELLIGLEA 1014

QY 1028 ISEPDGKMRNVNANYNGQIRPMVRDRDRSVESVTATAEKADSNKNGHVAAPFAGVTVTV 1087

DB 1015 ISEPDGKMRNVNANYNGQIRPMVRDRDRSVESVTATAEKADSNKNGHVAAPFAGVTVTV 1074

QY 1088 AEGDEYKAGDAVAIEAMKMEATITASVDGKIDRVVPAATKVEGGDLIVVWS 1140

DB 1075 CVGERVAGQTIATIEAMKMEATITASVDGKIDRVVPAATKVEGGDLIVVWS 1127

RESULT 8

Q50450

ID Q50450 PRELIMINARY; PRT; 1124 AA.

AC Q50450;

DT 01-NOV-1996 (TEMBLrel. 01, Created)

DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)

[illegible]


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Db 304 TMTGIDIVQSOIILADGCSLHSEVGIPEKQEDIRINGYAIQSRVITTEPDLNFMPTDG 363
QY 367 TITAYRSPGAGVRLD-GAAQLGGCTTAHFDMSLVKMTCKGSDGFVAVARAQALAEFTV 425
Db 364 KIMAYRSGGFGVRLDAGNGFOGAVITPYDSLLVLTWALTFEQAARKMLNLTFFL 423
QY 426 SGVANIGFLRALLREEDTSKRIANGFTIADHPLHLQAPDDEQGRILDIYADVTNPK 485
Db 424 RVFKTINPLENVHPKLSGEYDTSFTIDTPELVFPRKDRGFKMLTYIGTVNGVF 483
QY 486 HGVPRKDVAAPI---DKLENIKDL-PLPRGSRDLKQLGPAFAFARDLREODALAYDTTF 541
Db 484 PGIGKK--KKPVEDKPLKLSAEPIPGATQIOLDKHGPEGLVRIWQIPRVLTDTTF 541
QY 542 RDAHQSLLATRVRSFALKPAEAAVAKLPTPELLSVEAWGATYDVAMRFFLEDPWDRLDL 601
Db 542 RDAHQSLLATRVRTVDLVAEAPSARLLPNLSLEMMWGATEDVAVREFLKEDPWRLLKL 601
QY 602 REAMPNVNTQMLLRGNTVGYTPYDSCVRAFKENASGVDFIRFDALNDVQMRPAI 561
Db 602 RDAFPNVLFQMLRSANAYGYKNYPONVIREFVEKSAHAGIHFVFRIFDLSLNVKGMTVAI 661
QY 662 DAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYIKMAEIVKSGAHILAIKDMAGLLRP 721
Db 662 DAVRQSG-KIAEAAICYTGDIIDPSRSKYNLDYIKALAKELQAGAHILAIKDMAGLLRP 720
QY 722 AAVTKLVTLRREDFLVHVHTHDTAGGOLATYFAAAQAGADAVDGAASPALSGTTSQPSL 781
Db 721 QAAHVLISGLKETVDIPIVLHTDTSNGIGTYIYAKAIEAGVDIVDVAISSMAGLTSPSA 780
QY 782 SALVAFAFATRTDTGLSLEAVSDLEPYEAVRGILYLPFESGTPGPRGVYRHEIPGQLS 841
Db 781 NTLIYALEGTERAPEVDIYGLQELARYWEDVRKRFYOEFGSGMNAHPTEVHEMPGGQYS 840
QY 842 NZRAQATLGLADREFELIEDNYAAVNEMLGRPTKVTTPSSKVVGDGLALHLVAGVDPADFA 901
Db 841 NLQQAQKAVGLGRWDEKEMRYRNDLFGDIVKVTPTSSKVVGDGLALYVQNNLTQDIF 900
QY 902 ADQKYDIPDSVIAFLRGLGNPPGWPPELRLTRALEGRSEKAPUTEVPEEQAHLAD 961
Db 901 ERGETLNFDPDSVVELFEGYLGQPHGGFKELQRIILKGRE---PITVRPGELLEVPDPE 956
QY 962 D-SKERNLSNR-----LLPEKPTTEELHRRHRCGNTSALDDREFFGLVEGRET 1010
Db 957 QMKKEDYDLKRGVTDFAIAIALYALPKVFEVETVEKYGDVSVLDTPFTFLYGMRLGEET 1016
QY 1011 LIRLPDVRTPLVRLDAISEPDDKGMNRVYVANVNGQIRPMRVDRSVESWTATAEKAQSS 1070
Db 1017 EVEIERGKT-LIVKLVSIGQPQADGTRVYVYFELNGQPREWIRDESIKTAVVEHIKADRT 1075
QY 1071 NKGHVAAFPAG-VVTVVAGDEVKAGDAVAIEAMKMEATTITASVQGLDRVVVPAATK 1129
Db 1076 NFNHIAATMPGTVKVKVLYEKEGKVDKGDHLMVTEAMKMETTVQAPPAGVVKVYKSGDA 1135
QY 1130 VEGGOLLVYVS 1140
Db 1136 IQAGDILLMELS 1146

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RESULT 15

Q8Y846

ID Q8Y846 PRELIMINARY; PRT; 1146 AA.

AC Q8Y846;

DT 01-MAR-2002 (TEMBLrel. 20, Created)

DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)

DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)

DE PyCA protein.

GN PYCA OR LM01072

OS Listeria monocytogenes.

OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

OX NCBI_TaxID=1639;

RN [1]

9

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RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krefz J., Kuhn M., Kunst F., Kurapkat G.,
RA Madieno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordisiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RL "Comparative genomics of Listeria species.";
RT Science 294:849-852(2001).
DR EMBL; AL591977; CAC99150.1; -.
DR ListList; LM001072; -.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000089; Biotin_lipoyl.
DR InterPro; IPR005479; CPase_LD2.
DR InterPro; IPR005481; CPase_LN.
DR InterPro; IPR000891; HMGL-like.
DR InterPro; IPR003379; PYC_OADA.
DR InterPro; IPR005930; Pyruv_carbox.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; biotin_lipoyl; 1.
DR Pfam; PF00289; CPase_LD2; 1.
DR Pfam; PF02786; CPase_LD2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR TIGRFAMs; TIGR01235; pyruv_carbox; 1.
DR PROSITE; PS00866; CPASE_1; 1.
DR PROSITE; PS00867; CPASE_2; 1.
KW Complete proteome.
SQ
SEQUENCE 1146 AA; 128049 MW; A062F88C9A092B6F CRC64;

Query Match 43.1%; Score 2493; DB 16; Length 1146;
Best Local Similarity 45.8%; Pred. No. 2.2e-125;
Matches 526; Conservative 185; Mismatches 408; Indels 30; Gaps 11;

QY 13 KKILVANRGEIIVRAFPRAALETGAATVAYIPREDGRSFHRSFASAEVRIGTEGSPVKAYL 72
Db 5 KKVIVANRGEIIVRAVWRACTELKIKTVAYSQEDTGSFHYKSDAEYLVGAGKKPIDAYL 64
QY 73 DIDEIIGAAKKADAIYGYGFLSENAQLARECAENGITFTGPTPEVLDTGDKSRAYT 132
Db 65 DIENITEIAKESGADAIHPGYGFLSENFIEFARRCEOGIIFVGPCKSHLDMFGDKIKAKE 124
QY 133 AAKKAGLPVLABST-PSKNIDEIVKSAEGQTVIFVKAVAGGGGGRGMRVVASPDELKILA 191
Db 125 QALLADIPVPGSNGPVAGIKVEEFGKNGPLMIKASIGGGGGRGMRVVESEKHEVKSF 184
QY 192 TEASREAAEAFDGGAVYVERVINPOHIEVQILGHTGEVHLYRDCSLQRHQQWVEI 251
Db 185 ERASSEAKAAGNDEVYVEKVMNPKHIEVQILGHTGHNIVHLFERDCSIQRRHQQWVEV 244
QY 252 APAQHLDPELRICADAVKFCRSIGYQAGIVEFLVDEKGNHVFEMNPRIQVEHTVTE 311
Db 245 AFCNAITSLRRICDAAVVKLMKNVDYINAGTVEFLV-EGDDFYFIEVNPVQVEHTITE 303
QY 312 EYTVEDLVKAOMRLAAGATLKELGLT---ODKIKTHGAALOCRIITEDNNNGFRPDGTGI 368
Db 304 MITGDIIVQSOLFIAQGYALHDLQVLAIPKQEDIHIGSAIQSRITTEPDLNFMPTDG 363
QY 369 TAYRSPGGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRSDGFETAVARAQALAEFTVSG 427
Db 364 DTYRSTGGFGVRLDAGNGFQGVTVVTFYDLSLVKLCTWGTMTFEQATKMRRLNIEFRING 423
QY 428 VATNIGFLRALLREEDFTSKRIATGFIADHPLHLQAPDDEQGRILDIYADVTNPKHG 487
Db 424 VKTINPFLNVVVRHDPDFASGNTYNTSIDTPELFPKPHIRDRGRTKTLRIGNVTYNGGFG 483

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3712.5	64.1	1127	2	D70671	pyruvate carboxyla
2	2541.9	43.9	1178	1	A47255	pyruvate carboxyla
3	2539.5	43.9	1178	2	J64391	pyruvate carboxyla
4	2525.5	43.6	1150	2	A39978	pyruvate carboxyla
5	2524	43.6	1148	2	F69685	pyruvate carboxyla
6	2517.5	43.5	1178	1	JC2460	pyruvate carboxyla
7	2493	43.1	1146	2	AH1208	pyruvate carboxyla
8	2491.5	43.0	1144	2	D97227	pyruvate carboxyla
9	2490	43.0	1146	2	AC1565	pyruvate carboxyla
10	2488	43.0	1150	2	G89881	pyruvate carboxyla
11	2473.5	42.7	1174	2	A52911	pyruvate carboxyla
12	2473.5	42.7	1174	2	C97686	pyruvate carboxyla
13	2464.5	42.6	1158	2	A53285	pyruvate carboxyla
14	2464	42.6	1175	2	T20346	pyruvate carboxyla
15	2457	42.4	1178	1	QY8YP	pyruvate carboxyla
16	2443	42.2	1185	2	T39734	pyruvate carboxyla
17	2436	42.1	1180	2	S46094	pyruvate carboxyla
18	2419	41.8	1195	2	T43735	pyruvate carboxyla
19	2406	41.6	1137	2	E86708	pyruvate carboxyla
20	2115.5	36.5	984	2	T44608	pyruvate carboxyla
21	1079	18.6	501	2	D64455	pyruvate carboxyla
22	1063.5	18.4	477	2	G70427	biotin carboxylase
23	1036.5	17.9	447	2	A53311	biotin carboxylase
24	1036.5	17.9	447	2	AH1923	biotin carboxylase
25	1035	17.9	472	2	A70432	biotin carboxylase
26	1019	17.6	506	2	D69277	biotin carboxylase
27	997	17.2	491	2	A69123	biotin carboxylase
28	981.5	17.0	448	2	S74380	biotin carboxylase
29	976.5	16.9	471	2	G82966	probable biotin ca

QY 192 TEASREAEAFGDCGAVYVERAVINPQHIEVQIILGHTGEVHLYVERDCSLQRHKKVVEI 251
 Db 182 EASREAEAFGDCPTVLEQAVINPQHIEVQIILGHTGEVHLYVERDCSLQRHKKVVEI 241
 QY 252 APAQHLDPPELRDRICADAVKFCRSIGYGAGTVEFLVDEKNGHVFIMNPRIOVEHTVTE 311
 Db 242 APAPHLDAELRYKMCVDVAFARHIGYSCAGTVEFLDERGEVVFIMNPRVQVEHTVTE 301
 QY 312 EVTEVDLVKQMLAAGATIKELGLTQDKTKTHGAALQCRITTEDPNNGRPDTGITAY 371
 Db 302 EITDVLVAVSOLRTAAGTELEQLRQEDTAPGGAALQCRITTEDPANGRPDTGRISAL 361
 QY 372 RSPGAGVRDLGAAQLGGLTAFHDSMLVMTKCGSDFFETAVARAQALAEFTVSGVATN 431
 Db 362 RTAGGAGVRDLGSGTNGAELSPFDVSMVLTGRDLPTAVARRARAIAEFTIRINGSTN 421
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 Db 422 IPFLQAVLDDPDRFAGRVTTSFIDERPQLLTARASADRGTKINFLADVTVNPNYGRSPS 481
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 Db 482 TI-YPDKLP---DLDLRAAPPAGSKORLVKLGPEGFARWLRESAAVGVVDTTFRDAHQ 537
 QY 548 LLATRVRSFALKPAAEAAVAKLTPELLSVEAWGATYDVAMREFEOPWDLDELREAMPN 607
 Db 538 LLATRVTSGLSVAPYLATMTQLLSVECGWATYDVALLUKEDPWERLATLRAAMPN 597
 QY 608 VNTOMLLRGRNTVGYTYPYDPSVCRAFVKEAASSGVDFRIFDALNDVSMRPAIDAVLET 667
 Db 598 ICLQMLLRGRNTVGYTYPYPIEIVTSFVQVQATATGIDIFRIFDALNNIESMRPAIDAVRET 657
 QY 668 NTAAVEAMAYSGDLSDPNEKLYTLDYVLLKMAEIVKSGAHILAIDKMGALLRPAATVKL 727
 Db 658 GSAIAEAMCYTGDLDTPGSQLTLDYVLLKMAEIVKSGAHILAIDKMGALLRPAATVKL 717
 QY 728 VTALRRREFDLPVHVHTHTDAGGOLATYFAAAQAGADAVDASAPLSGTTTSPSLSAVAA 787
 Db 718 VSALRSRFDLPVLHHTDTPGGQLASVAAWHAGADAVDGAAPLAGTTTSPALSSVAA 777
 QY 788 FAHTRRDTGLSLEAVSLEPYWRAVRLYLPPFSGTGPGRVYRHEIPGGQLSNLRAQA 847
 Db 778 AAHTYDTGLSLSAVCALEPYWRAVRLYLPPFSGTGPGRVYRHEIPGGQLSNLRAQA 837
 QY 848 TALGLADRFELIEDNVAANVEMLRPTKVTTPSSKVVGDIALHLVGAVDPAADPAQKY 907
 Db 838 TALGLDRFELIEEAVAGADRVLGRVKTPTTSKVVGDLALVLVGAVSADEASDPARF 897
 QY 908 DIPDSVTAFLRGELNPPGWPPEPLRTRALEGRSEKAPLTVPEEEQALHLDADDKERR 967
 Db 898 GIPESVLGRGELGDPGWPPEPLRTAALAGRAAR-PTAQLAADDEIALSSVGAK-RQ 955
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 Db 956 ATNLRLLFPKPTPEEFLEHREAYGDTSQLSANQFFYGLRQGEERVKL-ERGVELLIGLEA 1014
 QY 1028 ISEPDCKGMNVANVNGQLRPMVRDRVSVESTATAEKADSSNKGHVAAPFAGVTVTV 1087
 Db 1015 ISEPDCKGMNVANVNGQLRPMVRDRVSVESTATAEKADSSNKGHVAAPFAGVTVTV 1074
 QY 1088 AEGDEVKAGDAVAILIEMKMEATITASVDGKIDRVVVPAAATKGGGLIYVVS 1140
 Db 1075 CVGERVAGQTIATIEAMKMEAPITAPVAGTVVERVAVSDTAQVEGGDLIVVS 1127

RESULT 2

A47255

Pyruvate carboxylase (EC 6.4.1.1) precursor [similarity] - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Feb-2002

C:Accession: A47255

R:Zhang, J.; Xia, W.L.; Brew, K.; Ahmad, F.

Proc. Natl. Acad. Sci. U.S.A. 90, 1766-1770, 1993

A:Title: Adipose pyruvate carboxylase: amino acid sequence and domain structure deduc
 A:Reference number: A47255; MUID:93189578; PMID:8446588
 A:Accession: A47255
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1178 <HA>
 A:Cross-references: GB:109192; NID:g293743; PIDN:AAA39737.1; PID:g293744
 A:Experimental source: 3T3-L1 adipocytes
 C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl-biotin-bind
 C:Keywords: biotin binding; ligase; mitochondrion
 F:1-20/Domain: transit peptide (mitochondrion) #status predicted <TRP>
 F:21-1178/Product: pyruvate carboxylase #status predicted <WAT>
 F:39-494/Domain: biotin carboxylase homology <BCH>
 F:1105-1178/Domain: lipoyl-biotin-binding homology <LPB>
 F:1144/Binding site: biotin (lys) (covalent) #status predicted

Query Match 43.9%; Score 2541.5; DB 1; Length 1178;
 Best Local Similarity 47.0%; Pred. No. 9.4e-132;
 Matches 537; Conservative 187; Mismatches 401; Indels 17; Gaps 11;

QY 13 KKILVANRGETIAVRAFAALETGAATVAIYPREDGRGSHRSFASEAVRIGTEGSPVKAYL 72
 Db 38 KKVWANRGELIAIRVFRACTELGITRVAVYSEODTGOMHROKADAEVILIGRLAPQAYL 97
 QY 73 DIDEITGAAKVKADAIYPGYGSELSENAQLARECAENGITFTIGPTPEVLDLTGDKSRVAT 132
 Db 98 HIPDIILKVAKEGVDAVHPGYGSELSENAQLARECAENGITFTIGPTPEVLDLTGDKSRVAT 157
 QY 133 AAKKAGLPVL-AESTPSKNIDEIVKSAEGOTYPTFKAVAGGGGRGMRFFVASPEDELRKLA 191
 Db 158 IATAAGVVPVPGTDSPLSSISHEAHEFSNTGFPILFKAAVGGGGRGMRVHVHSEELSENY 217
 QY 192 TEASREAEAFGDCGAVYVERAVINPQHIEVQIILGHTGEVHLYVERDCSLQRHKKVVEI 251
 Db 218 TRAYSEALAAFGNGALFVEKFIKPRHIEVQIILGHTGEVHLYVERDCSLQRHKKVVEI 277
 QY 252 APAQHLDPPELRDRICADAVKFCRSIGYGAGTVEFLVDEKNGHVFIMNPRIOVEHTVTE 311
 Db 278 APATHLDPQLRSRLTSDSVKLAKQVGYENAGTVEFLVDEKNGHVFIMNPRIOVEHTVTE 337
 QY 312 EVTEVDLVKQMLAAGATIKELGLTQDKTKTHGAALQCRITTEDPNNGRPDTGITAY 371
 Db 338 EITDVLVAVSOLRTAAGTELEQLRQEDTAPGGAALQCRITTEDPANGRPDTGRISAL 397
 QY 372 RSPGAGVRDLGAAQL-GGEITAFBDSMLVKMTCRGSDFFETAVARAQALAEFTVSGVAT 430
 Db 398 RSGEGMGRIRLDNASAFQGAIVSPHYDLSLVKVIAHGKDHPTAATKMSRALAEFRGVKT 457
 QY 431 NIGFLRALLEDEFTSKRIATGFIADHPLHLLQAPADDEQGRILDYADVTNPKPHGRPK 490
 Db 458 NIPELQNLVNNQQLAGTVDTQFIDENPELFLQRPQNRAQKLLHLVGHVWVNGPTTPIP 517
 QY 491 KDVA-APID-KLPNIKDLPLPRGSRDLKQLGPAFARLREODALAVTDTTFRDAHQSL 548
 Db 518 VNVSPSPVDPAVPVPIGPPGAFRDLILREGPEGFARAVRNHQLGLLMDTTFRDAHQSL 577
 QY 549 LATRVRSFALKPAAEAAVAKLTPELLSVEAWGATYDVAMREFEOPWDLDELREAMPN 608
 Db 578 LATRVTRHDLKLTAPYVAHNFNLFSMENMGATFDVAMRFLYECPRWRLQELRELIPNI 637
 QY 609 NIQMLLRGRNTVGYTYPYDPSVCRAFVKEAASSGVDFRIFDALNDVSMRPAIDAVLETN 668
 Db 638 PFQMLLRGANAVGTYINPDNVKFCVAKENGMDFRVFDSUNYLPNMLLGEAAGSAG 697
 QY 669 TAAVEAMAYSGDLSDPNEKLYTLDYVLLKMAEIVKSGAHILAIDKMGALLRPAATVKL 728
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 QY 729 TALRRREF-DLPVHVHTHTDAGGOLATYFAAAQAGADAVDASAPLSGTTTSPSLSAVAA 787
 Db 757 SSLRDRFPDLPVHVHTHTDAGGOLATYFAAAQAGADAVDASAPLSGTTTSPSLSAVAA 816

Db 973 RIEGRPGASPLLNKLEKDLIDRHEEVIPEVDLSAAMPVDFVAFKDFKDTATFGPLDS 1032

Qy 995 LDRREFFYGIVGEGRETLIRLDPVATPLLRDLAISEPDDKMRNVANVAGQIRPMRYRD 1054

Db 1033 LNTRLFQGPKIABEFVELEGRKT-CHIKALAVSDLNRAQGVFFELNGQLRSILVKD 1091

Qy 1055 RSVESVATAEKADSSNKHGVAAPFAG-VVTYVVAEGDEKAGDANVAIIAMKMEATITA 1113

Db 1092 TQAMKEMHFHPKALKDKYKGIGAPMGKVDVKVAAAGAKVKGQPLCVLSAMKMETVYTS 1151

Qy 1114 SVDGKIDRVVPAATKVEGGDLIVV 1139

Db 1152 PMESTIRKVVTKDMTEGGDLILEI 1177

RESULT 4

A83978

pyruvate carboxylase pyca [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: A83978

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: A83978

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1150 <STO>

A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BA06344.1; GSPDB:GN00

A;Experimental source: strain C-125

C;Genetics:

A;Gene: pyca

C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 43.6%; Score 2525.5; DB 2; Length 1150;

Best Local Similarity 46.8%; Pred. No. 6.9e-131;

Matches 539; Conservative 185; Mismatches 400; Indels 27; Gaps 13;

Qy 9 LPFAKKILVANRGEIAVRAFRALETGAATVAIYPRDRGSHFRSFRASEAVRIGTEGSPV 68

Db 4 LKNIKKLVANRGEIAIRIPRACTELHIRTVAIYSKEDTGAYHRYKADEAYLVGEGKKPI 63

Qy 69 KAYLDEIDETIGAAGKVKADAIYGYGFLSENAQLARECAENGITFTGPTPEVLDTGDKS 128

Db 64 EAYLDIEGIEIAKRGVDIAHGYGFLSENFIAKRCHEEGIIIFIGPELEHLVIMFGDKV 123

Qy 129 RAYTAAKKAGLPLAEST-PSKNIDEIVKSAEGQTYPIFKVAVAGGGGGRGMRVFASPD 187

Db 124 QAREQAIAKALNPVPGSDGVPSSLEDVKAFAKADKHGYFFIIKAALGGGGRGMRVRSNDV 183

Qy 188 RKLATEASRAEAAGFGVAVYVERAVINPOHIEVQILGDTIGEVHLYERDCSLQRHQK 247

Db 184 QESYERAKSEAKAAGFNDVYVSKFIENPKHIEVQILADKHGNTLHLYERDCSVQRHQK 243

Qy 248 VBIETAQHLDPDLORICADAVKFCRSIGYAGAGYFVFLVDEKGNHVFTEMNPRIOVEH 307

Db 244 VVEVASVLSLSDVREIRICQAAVQLAENVVNVAGTVEFLVDREGNYFIEVNPQVEH 303

Qy 308 TVTEVTEVDLVKAQMLAAGATL--KELGL-TQDKIKTHGAALQCRITTEDPNNGFRPD 364

Db 304 TITEMVTGIDIVQSOLFADGEHLHGRDGLGIPKQEEIIVCHGYALQSRVTTEDPSNGFLPD 363

Qy 365 TGITAYRSGGAGVRLD-GAALGGEITAFHFSMLVKTGCRSDSETAVARAQALAEF 423

Db 364 TGRINAYRSGGGFVRLDAGNGFQAGVITPYDLSLLVKSVTWALTTEGAARKMLNREF 423

Qy 424 TVSGVATNIGFIRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYADTVN 493

Db 424 RINGIKTNIAFLENVQVHROFLSGEYNTSFIDQTPELFVFPKKRDKRGTKMLSFIGETIV 493

Qy 484 KPGVAPKDVAAPIDK--LPNIK-DLPLPRGSRDLKQLGPAFAFADRLREQDALAVTDTT 540

Db 484 GYPCLE-KTKKVPDKPPVKLKLSEPIPGCTKOILDQHGPEGLAKVWKQKHVLLDNT 542

Qy 541 FROAHQSLLATRVRSFALKPAEAAVAKLTPELLSVEAWGGATYDVAMRFEDFPDWRUDE 600

Db 543 FROAHQSLLATRVTHDKLQIAEPTARLLNPLFSMEMWGGATFDVAMRFLEDHEDWERILLI 602

Qy 601 LRAMPWNNTOMLIRGNTVGYTYPDSVCRFAFVKEAASSGVDIFRIFDALNDVQMRPA 660

Db 603 LRKAPNVLQMLLRASNAVGYKNYPDNLIRFEVDKSNAGIDVFRIFDLSINWVEGKMLA 662

Qy 661 IDAVLETNTAVAEVAMAYSGDLSDPNEKLYTLDYILKWAEEIVKSGAHIIAIDMAGILLR 720

Db 663 IEAVGEAN-KIAEATICYTGDIILSSRPKYDLYAYKKLAKELEAAGAHIIIGIKDMAGILLK 721

Qy 721 PAAVTKLVTALRRFEEDLVFVHVHTDTAGGQIATYFAAAQAGADAVDAGASAPLSGTTSQPS 780

Db 722 PEAAQIQLVAELKDTVTIPVHLHTDTSNGIFTYARAIEAGVDIVDVAVSSMAGLTQSPS 781

Qy 781 LSAIVAAFAFATRDYTGSLSEAVSDLEPYWEAVRGLYLPFSGTPGPTGRVYRHEIPGQL 840

Db 782 ANSLYALADSEKQPNVNITALEQLAEFWEETKFKYAGFESGMNAPHTVEYHEMPPGGY 841

Qy 841 SNLRQAOTALGLADRFELIEDNVAAVNMELGRPTKVTTPSSKVVGDIALHLVAGVDPADF 900

Db 842 SNLQOQAKAVGLGHRNVEKMYRTVNDMGDVVKVTPSSKVVGDIALYVQNDLTFEEV 901

Qy 901 AADPKYDIPDSVIAFLRGLNPPGGWPEPLRTRALEGRSEKAPLTPVEPEEQALHDA 960

Db 902 YENGKLDLDFDPSVVEFFEGQGPYQGFKKLQEIILKGRK----PITNRPGENMPEIQF 957

Qy 961 DDKER-RNSLR-----LLPKPTEELEHRRREGNTSALDDREFFYGLVVEGRE 1009

Db 958 EAIKEELYNKLDKQVTSHTDLSYALPKVFMFEERFQTEGDSVLDTPFTFFVGLRPGEE 1017

Qy 1010 TLIRLPDVRTPLLRLDAISEPDDKMRNVANVAGQIRPMRVDRSVESVTATAEKAS 1069

Db 1018 IEVEIEQGT-LIVKFLISLSKPODDGNRIYVVELNGOPREVLKQDSVKTSIIRPKADK 1076

Qy 1070 SNKGHVAAPFAG-VVTYVVAEGDEKAGDAVAIIAMKMEATITASVDGKIDRVVPAAT 1128

Db 1077 SNEPHIGASPGTWTWALVEKGVKQGDHLMITEAMKMETTVAQPDGGEVVAHVKDGD 1136

Qy 1129 KVEGGDLIVV 1139

Db 1137 AIQTGDLILIEV 1147

RESULT 5

F69685

pyruvate carboxylase (EC 6.4.1.1) pyca [similarity] - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 18-Aug-2000

C:Accession: F69685

R;Kunst, S.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Allioni, G.; Azevedo, V.; Per

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M

Koetter, P.; Koningshten, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanl

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Se

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terstra, P.; Tognoni, A.; Tosato, V.; Uchiya

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yasumoto, K.; Yasumoto, K.; Yata, K.; Yoshida

A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili

A;Reference number: A63580; MUID:98044033; PMID:9384377

A;Accession: F69685

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-1148 <KUN>

C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
F:8-465/Domain: biotin carboxylase homology <BCH>
C;Keywords: ligase
F:1073-1146/Domain: lipoyl/biotin-binding homology <LPB>
F:1112/Binding site: biotin (Lys) (covalent) #status predicted

0v 11 AEFKTLIVANPCETAVDAEPBAI ETCALMIVATVDDDDCCCEHDCB CNAINTCETCCNWA 70

QY 71 YLDIDELIGAAKKVKADAIYPGYGFSENAQLARECAENGITFIGPTPEVLDLTGDKSRA 13

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QY
I3I VTAAKAGLPVLAEST-PSKNIDEIVKSAEQGYPIFVKAVAGGGGMRFEVASPDLRK 189
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Db 185 AYERAKSEAKAAGFNDEYVVEKLIENPKHIEVOVIGDKOGNYYHLFERDCSVORRHOKYT 244

Db 245 EVAPSVLSPELRDQICEAAVALAKNVNINAGTVEFLV-ANNEFYFIEVNPVQVEHTI 303

Db 304 TEMITGVDIVQTQLLVAQGHSLHKKVNIPEQKDIFTIGYALQSRVTTEDPQNDMPDIG 363

0A SCVATNICEI PAII ENBDEMECVBIAMONTAINDUUY OABDADNDGCGCTE VNS E DZUMVVV
436
001 AAAAAAAAGGGGGT GVAEDJIGNST QGAV IIFIIDSLVLKLSIWALIFEQAAAANRVKNLQEFKL 423

QY 484 -----KPHGVRPXDAAPIDKIPNICKDLPIPGSRDLKQLGPAFAFDLREQDALAV 536

QY 537 TDTTFRDAHQSLLATVRVSFALKPAAAEAVAKLTPELLSVEAWGGATYDYAMRFLFEDPWD 596

QY KEDELEAMFNVNIQMLGRNRNVGTYPTYPDSVCRAEVREAASSGVDFRIFDALNDVSQ 656

Db

657 MTLAIDAVRDTG-KVAEAAICTGDIILDKNRTKYDILAVTYSMAKELEAAAGAHIIIGKMA 715

Db 716 GLLKQAAAYELVSALKETIDIPVHLTHDTSNGIYMYAKAVEAGVDIIDVAVSSMAGLT 775

Db 776 SQPSASGFYHAMEGNDRRPEMNVQGVLLSQIWESVRKYYSEFESGMKSPHTEIYEHEMP 835

[illegible]

D0 896 EKDVYKESLDFDSVVELFKGNIGQPHGFPPEKLQKILKGQE---PITVRPGELE 951

952 FVSEAIKQEFKEQHNEISD---QDAVAYALYPRVFTDYVTKTYESYGDISVLDTPTF 1007

QY 1062 ATA EKADSSNKGHVAAAPFAGVVTVTVAE-GDEVKAGDAVAIIEMKMEATITASVDGKID 1120

QY 1121 RVVPAAATKVEGGDLIVV 1139

RESULT 6

C:Species: Homo sapiens (man)
C:Date: 10-Sep-1988 #sequence
C:Name: Pyruvate:carbon dioxide lyase (ADP forming)
C:Revision: 19-Aug-2000 #start change: 01-Feb-2003

submitted to the ENBL Data Library, July 1995
A; Reference number: H00708

A;Residues: 1-1178 <WAL>
A;Cross-references: EMBL:P10891; NID:J1101028; PDB:AAA82937 1. PDB:J1101029

A: title: cDNA cloning of human kidney pyruvate carboxylase.
A: reference number: JC2460; MUID: 94324922; PMID: 8048912

A:Cross-references: GB:S72370; NID:g632807; PIDN:AAB31500.1; PID:g632808
R:Lamhonwah, A.M.; Quan, F.; Gravel, R.A.

A: Accession: B27883
A: Reference number: AZ/663; M01D:61212031; F01D:3333346
A: Molecular function: RNA

R. Freytag, S.O.; Collier, K.J.
J. Biol. Chem. 259, 12831-12837, 1984

A: Status: preliminary
A: Molecule type: mpna
Accession: 00102

C:Genetics:
A:Gene: GDB:PC

C;Keywords: biotin binding; gluconeogenesis; ligase; mitochondrion
F;1-20/Domain: transit peptide (mitochondrion) **!status predicted** **<TND>**

F:II05-11/8/Domain: lipoyl/biotin-binding homology <LPB>
F:II44/Binding site: biotin (Lys) (covalent) #status predicted

QY	1000	FFTGVLVEGRITLLRFDVTRTPLLRLDAISEPDDKGMNVNVANVNGOIRPMVRDRSVES	1059		
Db	1038	FLAGPKIAEEFFVELEERKGT-LHIKALAVSDLNRAGQORQFFELINGQLRSILVKDTQAMK	1096		
QY	1060	VTATAKADSSNGHVAAPFAG-VVTVTVAEGDEVKAGDAVAIIEMKMEATITASVDGK	1118		
Db	1097	EMHFHPKALKDVGQIGAPMPGKVIDIKVVAGAKVAKGQPLCVLSAMKMETVVTSPMEGT	1156		
QY	1119	IDRVVVPAAATFKVEGGDLIVVV	1139		
Db	1157	VRKVHTKMDTLEGGDLILEI	1177		
RESULT 7					
AH1208					
pyruvate carboxylase homolog pyca [imported] - Listeria monocytogenes (strain EGD-e)					
C:Species: Listeria monocytogenes					
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001					
C:Accession: AH1208					
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec					
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,					
Science 294, 849-852, 2001					
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;					
Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla					
A:Title: Comparative genomics of Listeria species.					
A:Reference number: AB1077; MUID:21537279; PMID:11679669					
A:Accession: AH1208					
A:Status: preliminary					
A:Molecule type: DNA					
A:Residues: 1-1146 <GLA>					
A:Cross-references: GB:NC_003210; PIDN:CAC99150.1; PID:g16410474; GSPDB:GN00177					
A:Experimental source: strain EGD-e					
C:Genetics:					
A:Gene: pyca					
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bind					
Query Match	43.1%;	Score 2493;	DB 2;	Length 1146;	
Best Local Similarity	45.8%;	Pred. No. 4.2e-129;			
Matches	526;	Conservative 185;	Mismatches 408;	Indels 30;	Gaps 11;
QY	13	KKILVANRGIAVRAFALETCGAATVAIYPREDRSFHSFASAVRIGTESPVKAYL	72		
Db	5	KKVLVANRGIAIRVWRACTELKIKTVIAYSQEDTSFHYKSDAEALYVGAGKKPIDAYL	64		
QY	73	DIDEITGAAKKVADAIYPGYFLSNAQALARECAENGITFTIGPTPEVLDLTDGKSRVAT	132		
Db	65	DIENTIETAKESGADAIHPGYFLSENTEFARRCQEGIIIFVGPCKSLHDMFGDKIKAKE	124		
QY	133	AAKAGLPLVABST-PSKNIDEIVKSAEGQTYPIFKAVAGGGGGRMGREFVAPDELRKLA	191		
Db	125	QALLADIPIPGSNGPVAGIKEVEFEKNGYPLMIKASLGGGGRMGREFVAPDELRKLA	184		
QY	192	TPASREAAAFDGGVAVVERAVINPOHIEVQILGDRHTGEVHLVYERDCSLQRHOKVVEI	251		
Db	185	ERASSEAKAAFGNDEYVEKCVNPKHIEVQILGDRHTGNIVHLFERDCSIQRHOKVVEV	244		
QY	252	APAOHLPELDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFTEMNPRIQVEHTVTE	311		
Db	245	APCNAITSELNRICDAAVKLMKNVDYINAGVVEFLV-EGDDFYFIEVNPVQVEHTITE	303		
QY	312	EYTEVDLVKQMLAAGATLKELGLT---ODKIKTHGAALQCRITTEDPNNGFRDPTGTI	368		
Db	304	MITGIDIVQSOLFADGYALHDQLVAIPKQEDIHIGSAIQSKRITTEDPNNFMDPTGRV	363		
QY	369	TAYRSPGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTVSG	427		
Db	364	DTYRSTGGFVRLDAGNGCFQGTIVTPFYDSLVLKLTWGMTFEQATKMRNRLIEFRNG	423		
QY	428	VATNIGFTLRALLREDEFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLDATVKNPHG	487		
Db	424	VKTNPFLNVRHPDFASNGYNTSFIDTPELFKFPKPIRDRGKTKLRYIGNVTVNGPFG	483		

QY 1071 NKGHVAPRAG-VVTVVTAEGDVKAGADVAIVTEAMKMEATITASVDGKIDRVVVPAAK 1129
Db 1074 NKKEIGASIPGNVVKVFPKPKGKDSLMVTEAMKMETNVSVDGTVGGIFVKEGQ 1133
QY 1130 VEGGDLIV 1137
Db 1134 VQSGQLIV 1141

RESULT 9
AC1565
pyruvate carboxylase homolog pyca [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AC1565
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Esibi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueder, T.; Simoes, N.; Trierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1565
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1146 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC96291.1; PID:g16413519; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: pyca
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 43.0%; Score 2490; DB 2; Length 1146;
Best Local Similarity 46.0%; Pred. No. 6.1e-129;
Matches 528; Conservative 182; Mismatches 409; Indels 30; Gaps 12;

QY 13 KKLIVANRGEIAVRAFAALETGAATVAIYPRDGRSFHRSFASAVRIGTEGSPVKAYL 72
Db 5 KKLIVANRGEIAVRAFAALETGAATVAIYPRDGRSFHRSFASAVRIGTEGSPVKAYL 64

QY 73 DIDEITGAARKVADAIYPGYFLSNAOLARECAENGITFGPTPEVLDTLTKSRVIT 132
Db 65 DIENIEIAKESGADAIHPGYFLSENIEFARCEGEGIFVGPCKSHLDMFGDKIKAKE 124

QY 133 AAKAGLPVLAEST-PSKNIDEIVKSAEGCTPIFVKAVAGGSGRMRVAPDELKLA 191
Db 125 QALLADIPVPGSDGSPVAGIKEVEFEKNGYPLMIKASIGGGGRMRVSVESKEHVESF 184

QY 192 TEASREAAAFDGVAVYVERAVINPOHIEVQILGDHTEGVHLYERDCSLQRHOKVVEI 251
Db 185 ERASAKAAGFNDVEYVEKVNPHIEVQILGDTHGNIVHLFERDCSIQRHOKVVEV 244

QY 252 APAQHLDPELRICADAVKFCRSYQYAGTVEFLVDEKGNHVFTEMNPRIQVEHTVPE 311
Db 245 APCNAITSELNRICADAVKLMKNVDYINAGIVEFLV-EGDNFYFIEVNPVQVEHTITE 303

QY 312 ETEVDVLVAQMLAAGATILKELGLT---QDKIKTHGAALQCRITTEDPNNFRPDTGT 368
Db 304 MITGIDIVQSFLFIADGYALHQLVAIPKQEDTHIGSAIQSRITTEDPLNNFMPDTGRV 363

QY 369 TAYRSPGGAGVRLD-GAAQLGGEIATAHFDSMLVKMTCRSDPETAVARAQALAEFTVSG 427
Db 364 DYIRSTGGVRLDAGNGFGGVVTFYDSLLVVKLCTWGTTFEQATKMRNRLIEFRIG 423

QY 428 VATNIGFLRALLREEDFTSKRIATGFIADPHLLQAPPADDEQGRILDVADVTVMKPRG 487
Db 424 VKTNIPPELLNVVRHPDFASSNYSFTIDTPELFPFHIDRGTKTLRYIGNVTYNGVFG 483

QY 488 VRPKVAAPIDKLPNTKIDLP----LPRGSRRLKQLGPAFAFARDLREQDALAVDPTFRD 543
Db 484 IKRDE--KPYAEPRLPKIPYGSQIAPGTKQILDAKGPGGVVDVWVKQBEVLITDITLTD 541

QY 544 AHQSLLATRVSRPALPAAEAFAAKLPELISVWAGGATYDVAMRFLFEDPMDRLDELRE 603
Db 542 AHQSLLATRVSRKDIFQIADAMAHLPPNMFSEFMWGGATFDVAYRFLNEDPPVWRLTLR 601

QY 604 AMPNVNIQMLLRGRNTVGYTPYDPSVCRAPFVKEAASGVDFIFRIFDALNDVDSOMRAIDA 663
Db 602 QIPNVNMFQMLLRGANAVGKYNPDNVIREFVKSAQSGVDVFRVFDLSNWKMGVEYSIDA 661

QY 664 VLENTTAAEAMAYSGDLSDPNEKLYTLDDYLLKMAEEIVKSGAHIIATKDMAGLLRPA 723
Db 662 VREAG-KVVEATICYTGDIDDDTRTKYTDYKDMAKELVAQGTTHLIGKDMAGLLKPO 720

QY 724 VTKLVTALRREDFLVPHVHTHTAGQLATYFAAAQAGADAVDASAPLSGTTSPQSLSA 783
Db 721 AYRLIGELKTDVPTLHLDTHDTSNGIYTYAAASVAGVDIVDVASSAMSGATSQPSMTG 780

QY 784 IVAFAHTRDGSLSEAVSDLEPYWEAVRGLYLPFESGTPGTPGRVYRHEIPGGQSLNL 843
Db 781 LYGLVNGRQTNLDNAQNSQIINHYYWEDVRHYKDFDNALNSQTEVYIHEMPGGQYTNL 840

QY 844 RAQATALGLADRELELLEDNYAAVNEMLGRPTKVPSSKVVGDALHLHVGAGVDPADFAAD 903
Db 841 QQQAIAVGLDRWDEVKMYVTVNQMGDIVKVPSSKVVGDALHFMVQNELTEEDVYEK 900

QY 904 POKYDIPDSVIAPLRGELNPGGWPPELTRALEGRSEKAPLTEVP-----EEE 954
Db 901 GDTIDPDSVIEFFMGIEGQYGGFPEKLQKLVKGT---PLADRPGLMPEVNFV 956

QY 955 QAHLDAADSKE--RRNSLNLFFPKTEFLEHRRRFGNTSALDDREYFGLVEGRETLL 1012
Db 957 KALKEKMGYSEKDVISILYKVFVDYQEMISKYGDVTVLDTTFFKGMRLGETIEV 1016

QY 1013 RLPDVETPLLRDLDAISEDDKGMNVANVANQIRPMRVDRSVESVATATAEKADSSNK 1072
Db 1017 ELEKGTI-LLIKLSIGEPIADGTRVYFELNGQPREINIQMNVOSTVIARRKIDTNP 1075

QY 1073 GHVAAPFAG-VVTVVTAEGDEVKAGDAVALIEAMKMEATITASVDGKIDRVVVPAAKVE 1131
Db 1076 EHVGAITMTGSVQVVKVKGDSVKKGDPLLITEAMKMETTIQAFDFGSEVSIYVSDGTTIE 1135

QY 1132 GGDLIWVS 1140
Db 1136 SGDLIEVN 1144

RESULT 10
G89881
pyruvate carboxylase [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: G89881
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89881
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1150 <KUP>
A:Cross-references: GB:BA000018; PID:g13700915; PIDN:BA842211.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: pyca
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 43.0%; Score 2488; DB 2; Length 1150;
Best Local Similarity 45.2%; Pred. No. 7.9e-129;
Matches 527; Conservative 192; Mismatches 384; Indels 62; Gaps 14;

QY 13 KKLIVANRGEIAVRAFAALETGAATVAIYPRDGRSFHRSFASAVRIGTEGSPVKAYL 72
Db 13 KKLIVANRGEIAVRAFAALETGAATVAIYPRDGRSFHRSFASAVRIGTEGSPVKAYL 72

Db 557 EKRVLVDTTMRDGHQSLLATRVTHDIARVASVYSKALPQLLSECVGGATFDVSMRFL 616
QY 591 FEDPWRDLDELREAMPNNVNIOMLLGRNTVGYTPYDSVCRAFYKEAAASSGVDFRIFEDA 650
Db 617 TEDPWERLSLRREGAPNLLQMLLRGANGVGYKNYPDNVYFYVQAARGGVDFRVEDC 676
QY 651 LNDVSMQRPADAIVLETNATAVAEMAYSGDLSDPNEKLYTLDDYYLKMAREIVKSGAHL 710
Db 677 LNWENMRVSDAIAEEN--KLEAATICTVTDGLLNSARP KYDLKYTYNLNLALEKAGAHII 735
QY 711 AIKMAGLLRPAAVTKLVYALRRREFDLPVHVHTHTAGQOLATYFAAAQAGADAVDGASA 770
Db 736 AVKMAGLLKPAKAAKVFKAUREATGLPIHFHTHTDTSISAATVLAADVADGDAVDAAMD 795
QY 771 PLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGILYLPFESOTPGTGRV 830
Db 796 AFSGNTSQPCLGSIVEALSGSERDTGLDTEWIRRISEYWEAVRNOYAAFESDLKGPASEV 855
QY 831 YRHEIPGQSLNLRQAATALGLADRFELIEDNYAAYNEMLGRPTKVTPTSSKVVGDALHL 890
Db 856 YLHEMPGGQFTNLKQARSLSGLESKWHEVAQAYADANRMFGDIVKVTPTSSKVVGDALMM 915
QY 891 VGAGVDPADFAADPOKYDIPDSVIAFLRGELGNPPGWPPELRLTRALEGRSEGKAPLFEV 950
Db 916 VSQDLTVADVENPDREVSPDSVSMKGLDGLQSGPGWPEALOKKAL----KGEKPYIVR 971
QY 951 PEE--EQAHLDDADDKERRNSLNR-----LLFPKPTTEEFLEHRRRFGNTSALDDR 998
Db 972 PGSLELADLDA-ERKVIETKLERKVDDEFEFASYLMYPKVTDFALTAEYGPVSVLPTH 1030
QY 999 EFEYGLVSGRETLIRLPDVRTPPLVRLDAISEPDCKGMNVNANVNGQIRPMRVDRS-V 1057
Db 1031 AIFYGMEGDEELFADIERGKTLIVYN-QASSGIDDKGMVTFFVEINGOPRIKVPDRAGH 1089
QY 1058 ESVTATAKADSSNKGHVAAAPFAGVYT-VTVAESDEVKAGDAVAIIEMKMEATITASVD 1116
Db 1090 ASGSAVRKAEPGNASHIGAPMPGVISRVFNQOGEVAGDVLLSIEAMKMETALHAERD 1149
QY 1117 GKIDRVVVPAAKTVBGGDLIV 1137
Db 1150 GKIAEVLVKGQIDAKDOLLI 1170

RESULT 12
C97686
pyruvate carboxylase (U51439) [imported] - Agrobacterium tumefaciens (strain C58, Cereon
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-sep-2001 #text_change 18-Nov-2002
C:Accession: C97686
A.: Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouello, B.; Goldman,
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: C97686
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1174 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK88444.1; PID:gl5157941; GSPDB:GN00169
A:Gene: AGR_C4940
A:Map position: circular chromosome
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding

Query Match 42.7%; Score 2473.5; DB 2; Length 1174;
Best Local Similarity 46.6%; Pred. No. 5,le-128;
Matches 541; Conservative 173; Mismatches 406; Indels 41; Gaps 19;

QY 8 TLPAFKKILVANRGEIARAPRAALETGAATVAIYPRDRGSEFHSFASAEVRIG----- 62
Db 20 TVLKISKILVANRSEIARIVFRAANELGLKTVVAIWAEEKLSLHRFKADESVQVGGPHL 79
QY 63 -TEGSPVKAYLDIDEIIGAANKVKKADAIYPGYGFLSENQAARECAENGITFIGTPTEVL 121

Db 80 AKDMGPIESYLSIEEIVRAKISGADALHPGYGLLSPESEFVEACNKAIGITFIGTPOTM 139
QY 122 DLTGDKSRAVTAANKAGLPVLAESTP-SKNDEIVKSABQTYPIFVKAAGGGRGRNF 180
Db 140 POLGNKVAARNLAISVDVPVVPATNPLPDDLAERMAEEIGPYVMKASGWSGGGRMRA 199
QY 181 VASPDLEKLATEASREAAAFGAGVVERAVINPOHIEVQILGDHGTGEVVHLYERDCS 240
Db 200 IRKKEDLAREVTEAKREAAAFGDEVYLEKIVERARHVESQILGDTHGNVVHLFERDCS 259
QY 241 LORRHQKVETAPQAHLDELPRICADAVKFCRSIGYOGAGTVFELVD-EKGNVVFTEM 299
Db 260 IQRNKNKYVERAPAPYLSEAOQRQELAAYSLSKIAAATNIGAGTVBYLMDADTGKIFYFIEV 319
QY 300 NPTQVEHTVTEEVTEVDLVKAQMRLAAGATL--KELGL-TODKIKTHGAALQCRITTED 356
Db 320 NPTQVEHTVTEVGTGIDIVKAQHILEGAALGTAESGVPKQBDIRLNGHALQCRITTED 379
QY 357 PNNGFRPDTGITITAYRSPGGAGVRLD-QAAQLGGEITAHFDSMLYKMTCRSGDFETAVAR 415
Db 380 PEHNPIDYGRITAYRSASGFGIRLDGGTSYTGAVITRYDPLLVKVTAWAPEPDEAISR 439
QY 416 AQRALAEFTVSGVATNIGFLALLREEDFTSKRIATGFIADPHLLQAPPADDEOGRILD 475
Db 440 MDRALREFIRGIVATNLTFLEAIIIGHDSFRNNTYTRFIDSTPELFAOVKKQDRATKLLT 499
QY 476 YLADVTVN--KPHG-VRPKDVA--PIDKLNKIDPLPRGSRDRKLGKPAFAARDLRE 530
Db 500 YLADVTVNGHEPTEKRAKPAKAPI--VPYI-DAPTPDGTQKLLDKLPGKGFADWMRN 556
QY 531 QDAIATVDTTTRDAHQSLATRVRSFALKPAAEAVAKLTPELLSVEANGGATIDVAMRFL 590
Db 557 EKRVLVDTTMRDGHQSLLATRVTHDIARVASVYSKALPQLLSECVGGATFDVSMRFL 616
QY 591 FEDPWRDLDELREAMPNNVNIOMLLGRNTVGYTPYDSVCRAFYKEAAASSGVDFRIFEDA 650
Db 617 TEDPWERLSLRREGAPNLLQMLLRGANGVGYKNYPDNVYFYVQAARGGVDFRVEDC 676
QY 651 LNDVSMQRPADAIVLETNATAVAEMAYSGDLSDPNEKLYTLDDYYLKMAREIVKSGAHL 710
Db 677 LNWENMRVSDAIAEEN--KLEAATICTVTDGLLNSARP KYDLKYTYNLNLALEKAGAHII 735
QY 711 AIKMAGLLRPAAVTKLVYALRRREFDLPVHVHTHTAGQOLATYFAAAQAGADAVDGASA 770
Db 736 AVKMAGLLKPAKAAKVFKAUREATGLPIHFHTHTDTSISAATVLAADVADGDAVDAAMD 795
QY 771 PLSGTTSQPSLSAIVAAFAHTRRDTGLSLEAVSDLEPYWEAVRGILYLPFESOTPGTGRV 830
Db 796 AFSGNTSQPCLGSIVEALSGSERDTGLDTEWIRRISEYWEAVRNOYAAFESDLKGPASEV 855
QY 831 YRHEIPGQSLNLRQAATALGLADRFELIEDNYAAYNEMLGRPTKVTPTSSKVVGDALHL 890
Db 856 YLHEMPGGQFTNLKQARSLSGLESKWHEVAQAYADANRMFGDIVKVTPTSSKVVGDALMM 915
QY 891 VGAGVDPADFAADPOKYDIPDSVIAFLRGELGNPPGWPPELRLTRALEGRSEGKAPLFEV 950
Db 916 VSQDLTVADVENPDREVSPDSVSMKGLDGLQSGPGWPEALOKKAL----KGEKPYIVR 971
QY 951 PEE--EQAHLDDADDKERRNSLNR-----LLFPKPTTEEFLEHRRRFGNTSALDDR 998
Db 972 PGSLELADLDA-ERKVIETKLERKVDDEFEFASYLMYPKVTDFALTAEYGPVSVLPTH 1030
QY 999 EFEYGLVSGRETLIRLPDVRTPPLVRLDAISEPDCKGMNVNANVNGQIRPMRVDRS-V 1057
Db 1031 AIFYGMEGDEELFADIERGKTLIVYN-QASSGIDDKGMVTFFVEINGOPRIKVPDRAGH 1089
QY 1058 ESVTATAKADSSNKGHVAAAPFAGVYT-VTVAESDEVKAGDAVAIIEMKMEATITASVD 1116
Db 1090 ASGSAVRKAEPGNASHIGAPMPGVISRVFNQOGEVAGDVLLSIEAMKMETALHAERD 1149
QY 1117 GKIDRVVVPAAKTVBGGDLIV 1137
Db 1150 GKIAEVLVKGQIDAKDOLLI 1170

Db 1150 GKAEVLVKGQDIDAKDLII 1170

RESULT 13
AE3285

pyruvate carboxylase (EC 6.4.1.1) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: AE3285

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, E.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688

A;Accession: AE3285
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1158 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL51448.1; PID:gl7982157; GSPDB:GN00190
A;Experimental source: strain 16M

C;Genetics:
A;Gene: BMEI0266
A;Map position: I
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
C;Keywords: ligase

Query Match 42.6%; Score 2464.5; DB 2; Length 1158;
Best Local Similarity 46.6%; Pred. No. 1.7e-127;
Matches 538; Conservative 171; Mismatches 408; Indels 37; Gaps 15;

QY 14 KILVANGETAVRAFAALETGAATVAIYPRDRGSHRSFASAEVRIQ-----TEGSP 67
DB 10 KILVANSEIAIRVFAANLGLKTVTIWAEEKLSLHREKADSEYQVGRGPHLDRLG 69
QY 68 VYALDIDETIIGAIAKVKADAIYPGYGFLENQAQARECAENGITFPGTPPEVLDITGDK 127
DB 70 IESYLSIDEIIRVAKLSGADAIHPGGLLSEFEFAEACAENGIVTIGPKPTMRLGNK 129
QY 128 SRVATAAKKAGLPVLAESTP-SKNIDEIVKASBGQTYPIPVKAVAGGGGRGMFVASPDE 186
DB 130 VAARNLAIEIGVVPVATDPLPDDDEVKLAQIGVPLMKASWGGGGRGMRAIRAEAD 189
QY 187 LRKLAETASREAAFGDAGVYVERAVINPQHTEVQILGDHTGEVHLVFERDCSLORRHQ 246
DB 190 LAREVMEAKREAAAFKGEVLEKLVERRARVEVQILGTYGNVHLFERDCSIORRNQ 249
QY 247 KVVEIAPAHLDPMLDRICADAVKFCRSIGYOGAGTVEFLVD-EKGNHVFIEMNRIQV 305
DB 250 KVVERAPAPYLNDQARRELADYGLKTAHATDYIGAGTVEFLMDADTGKFFIEVNPRIQV 309
QY 306 EHVTVTEVTVDLVKAQMLIAAGATL--KELGL-TQDKIKTHGAALQCRITTEDPNNGR 362
DB 310 EHTVTEVTGIDIVKAIHLEGAFTGTPESGVPRQEDIRLNHALQCRITTEDPEQNF 369
QY 363 PDGTGTTAVSPGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGSDFFETAVARAORALA 421
DB 370 PDGRIQATNSAAGFGIRLDGGGAYSGAFITRYDPLLVKVTASGATPLEAIHRMDRLR 429
QY 422 EFTVSGVATNIGFLRALLREEDFTSKRIATGFTLADHPHLLQAPPADDEQRIIDLADVT 481
DB 430 EPRIGVATNLTFEALINHPKFLSNDYTRFIDTTPPEFQMKRODRATKLLITYADVT 489
QY 482 VN-----KPHGVPRKQVAAPIDKLPNKIDLPGRGSRDRILKQLGPAFAARDLREQDALAV 536
DB 490 VNGHPETKGRAPARAAPK--RVPWFGDKLVADGTQKLLDQLGPKKFAEWMNRKRALI 547
QY 537 TDITFDAGHOSLLATVRVSFALKPAEAENAKLTPELLSVANGGATYDVAMRPLFDPDWD 596
DB 548 TDITMDGHOSLLATVRVYDIARIANAQAALPNLFLSECGWGGATFDVSMRLETDPWE 607
QY 597 RLDELREAMPNVNIOMLLRGNVTGYTPYDPSVCFRAVKEAASGGVYDIFRIDALNDVQ 656
DB 608 RLALVREGAPNLLQLMLGANGCVGYKSPDNDVVKYFVREARAGIDLFRVFDLSNWNEN 667

QY 657 MRPAIDAVLEINTAVAEVAMAYSGDLPNEKLYTLDYILKMAEEIYKSGAHILAIKDMA 716
DB 668 MRVSMADVLEEN-KLCEAAICYGDIINPRAKTDLNIYVNLAKEVEKAGHILAVKDMA 726
QY 717 GLLRPAAVTKLVTLRRREFDLPVHVHTDTHAGGOLATYFAAAQAGADAVDASAPLSGTT 776
DB 727 GLLKPAARVLFKALREETDLPHTFHTDTSIGISAATVLAADAGVDVDAAMDALSNST 786
QY 777 SOPSLSAIVAAFAHTRDTGLSLEAVSDLEPYWEAVRGLYLPRESGTPGPTGRVYRHIIP 836
DB 787 SQPCLSIVBALRGSEDSGLDPLIRISFYWEAVRHOYAFAESDLKGPASEVYLHEMP 846
QY 837 GGQLSNLRQAQATGALGLADREFELTDNVAAYNMLGRPTKVTPTSKVYDGLALHLVAGVD 896
DB 847 GGQFTNLKEQARSGLLETRHVEYAQAADVNRMGDIVKVTPTSKVYDGLALHLVAGVD 906
QY 897 PADFAADPQKYDIPDSVIAFLRGELNPPGCGWPEPLTRALEGRSEKAPLVEYPER--E 954
DB 907 VADVENPAKDIAFPDSVVMRMGDLGQPPSGWPEALQKVL---KDEKPTVVRPGSLLP 962
QY 955 QAHLDA-----DQSKERNSS---LNRLLPKPTTEEFLEHRRRFGNTSALDDREFFGLV 1005
DB 963 AALDAERKSFEDSVGKGLSDQEFASALMYPKVTDTATAHETYGPTSVLPTVPIFYGLK 1022
QY 1006 EGRETLIRLPDVRTPLLVRLDAISEPDDKGMNVVANVNGOIRPMRVDRSRESVATAE 1065
DB 1023 PESEVFDLBERGKTLIVN-QAMSEIDKGMVTVFFELNGQPRIKVPNRAKAGSGVRR 1081
QY 1066 KADSSNKGHVAAPFAGVV-TVTVAEGDEVKAGDAVAIIIEAMKMEATITASVDGKIDRVVV 1124
DB 1082 KVEAGNDKQVAGPMPGVISTVAVVAGQVTOGDVLLSIEAMKMETAIHAEROGTIAEVLV 1141
QY 1125 PAATKVEGGDLIVV 1138
DB 1142 RQGEQIDAKDLII 1155

RESULT 14
T20346

pyruvate carboxylase (EC 6.4.1.1) D2023.2 [similarity] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
C;Accession: T20346
R;Kershaw, J.
submitted to the EMBL data Library, October 1996
A;Reference number: Z19260
A;Accession: T20346
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1175 <WIL>
A;Cross-references: EMBL:Z81052; PIDN:CAB02872.1; GSPDB:GN00023; CESP:D2023.2
A;Experimental source: clone D2023
C;Genetics:
A;Gene: CESP:D2023.2
A;Map position: 5
A;Introns: 34/3; 103/3; 246/1; 451/3; 567/2; 821/1; 1045/3; 1126/3
C;Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
C;Keywords: ligase
F;1140/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 42.6%; Score 2464; DB 2; Length 1175;
Best Local Similarity 45.2%; Pred. No. 1.7e-127;
Matches 523; Conservative 200; Mismatches 389; Indels 46; Gaps 14;

QY 12 FKKILVANGETAVRAFAALETGAATVAIYPRDRGSHRSFASAEVRIQTEGSPVKAY 71
DB 32 FNKVMVANGETAIRVFRALTEINKTSVAIYAEQDKNSMRLKADAEYLVGKGLPVAAY 91
QY 72 LDIDEIIGAIAKVKADAIYPGYGFLENQAQARECAENGITFPGTPPEVLDITGDKSRV 131
DB 92 LTIDQIETALKHNIDAIHPGYGFLSERSDFAAACQAGIVFGPSPDVWARMGDKVAAR 151

QY	132	TAAKKAGLPUAEST-PSKNIIDEIVKSAEGTQYIFVKAVAGGGGRMRFVAPSDERKL	190
DB	152	QAALAEAGVQVPGTPITTADEAVEFAKQYGTILILKAAAYGGGGRIRRVDKLEEDEA	211
QY	191	ATEASREAAAFGDGAVVERAVINPOHIEVQILGDHTGEVVHLYERDCSLORHQKVE	250
DB	212	FRRSYSEAAAFGDGSLFVEKVERPHRIEVQILGDHGNLVHLIERDCSVORRHQKVE	271
QY	251	IAPAQHLDELURDICADAKFCRSIGSYQGAGTVEFLVDEKGNHVFIEIENPRIQVHTVT	310
DB	272	IAPAPALPEGVREKILADALRLARHVGYNAGTVEFLVDQKGNIFYEVNARLOVHTVT	331
QY	311	EEVTEVDLVKAQMLAAGATILKELGLTQDKTKTGAALQCRITTEDPNNGRPDGTITA	370
DB	332	EEITGVDLVQAQIRIAREKSLDDLUKLSQETITQTTGSAIQCRVTTEDPAKGQPSGRIEV	391
QY	371	YRSPGGAGVRLDGAQAQGGE-ITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVA	429
DB	392	FRSGEGMIRLDSASAFAGSVISPHYDSLVMKVITASARNHPNAAKMRALKKFRIGVK	451
QY	430	TNIGFLRALREEDFTSKRIATNGFIADHPLLQAPPADDEOGRILDYADVTKNP----	485
DB	452	TNIPFLNLVLRQPSFLDASVDTYIDBHPQLFQPKSQNRQAQLNLTLGEVKNGTPTPL	511
QY	486	HGVRPKDVAAPIDKLNINIKDLPRGSRORLKGPPAAAFARDLREODALAVTTTFRDA	544
DB	512	ATDLKPAVSPPIPIP--AGAKPTGLRDVLVORGTEFAKEVRSRPGCMITTITFRDA	569
QY	545	HQSLLATRVRSFALKPAEAVAKUTPELLSVEAGGATYDVAMRFLPEDPWRDLDEREA	604
DB	570	HQSLLATRVATYDMAAISPFAQFNGFLSLENNMGATFDVSMRFLHECPWERIQTIRKL	629
QY	605	MPNVNIQMLLRGNTVGYTPVPSVSCRAFYKEAASSGVDFRIPDALNDVYSQMRPADAV	664
DB	630	IPNIPFOCLLGGANAGSYNPDNVYIKFCELAVKNGMDVRFVDSLNYLPNLLVGMEAV	689
QY	665	LETNTVAEVAMAYSGDLSDPNEKLYTLDYLLKMAEEIVKSGAHLIAIKDMAGLLRPAAY	724
DB	690	GKAG-GVVEAAIAYTGOWTKSRDKYDLKYTLNLADQLVKAQAHLISIKDMAGVLKPEAA	748
QY	725	TKAVTALRRF-DLPVHVHTHTDAGGOLATYFAAAQAGADAVDGASAPLSGTSQSLSA	783
DB	749	KLJIGALURKFPDPIHVHTHTDSGGAAMLECAKAGADVDAVDSMGMTSQPSMGA	808
QY	784	IYAAFAHTRDGTGLSLEAVSDLEPYBVAWRGLYLPFSGTPGPGR--VYRHEIPGGOLS	841
DB	809	IVASLQGTKHTDGLSLDDISKYSAYWESTRLYAPFECATMTKSGNADVYKHEIPGGQYT	868
QY	842	NLRAQATAGLADRFELIENYAAVNDMLGRPTKVTPTSSKVGDALUHLVGAG-----V	895
DB	869	NLQQAFLSGLGQFDEVKRYREANVLGDITKVTPTSSKIVGDLAOFMYQNLLTRTLV	928
QY	896	DPADFAADPKYDIPDSVIAFLGELGNPPGGWPELUTRLEGRS--EGKAPLTPYEE	953
DB	929	DRAD-----DLSFPKSVDFMGNVQGPYPGPEPLTKVLRGKPKVDG-----PGE	976
QY	954	EQAHLDDASK-----ERRNSLRLLPKPTEEFLEHRRRGFNTSALDDREFFY	1002
DB	977	NAXPDLVDAVKVELEEKHGRTLSEEDVMSYSMEPTVFDEFETPRQOQGPVDKLPTRLFLT	1036
QY	1003	GLVEGRETLRLPDVTRPLVRLDAISEPDDKGMNRTVANVNGQIRPMRVDRDSVESVTA	1062
DB	1037	GLEIAEEDVIEESGKT-LAIQLLAEGLKNRGEREVFFDLINGQMRIFVVDKEASKEIV	1095
QY	1063	TAEKADSSNGHVAAPPAG-VVTVVAGDEVKAGDAVIAEAMKMEATITASVDGKIDR	1121
DB	1096	TRPALPGVRGHGAPMGPDVLELKIEGDKVTIKQPLFVLSAMKMEWIDSPAGTVKA	1155
QY	1122	VVYPAATKVBGGDLIVV	1139
DB	1156	IHAPOGTKCSAGDLVREV	1173

RESULT 15

QYBP

pyruvate carboxylase (EC 6.4.1.1) 1 [validated] - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein G3428; protein YGL062w; pyruvic carboxylase
C:Species: *Saccharomyces cerevisiae*
C>Date: 31-Dec-1991 #sequence revision 19-Jul-1996 #text_change 01-Feb-2002
C:Accession: S64066; A29233; S05760; A29722
R:Feuermann, M.; Potier, S.; Souciet, J.L.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64044
A:Accession: S64066
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-1178 <PEU>
A:Cross-references: EMBL:Z72584; NID:g1322565; PIDN:CAA96765.1; PID:g1322566; GSPDB:G
A:Experimental source: strain S288C
R:Lim, F.; Morris, C.P.; Occhiodoro, F.; Wallace, J.C.
J. Biol. Chem. 263, 11493-11497, 1988
A>Title: Sequence and domain structure of yeast pyruvate carboxylase.
A:Reference number: A92662; MUID:88298805; PMID:3042770
A:Accession: A29233
A:Molecule type: DNA
A:Residues: 1-461, G', 453-492, 'D', 494-594, 'A', 596-618, 'Q', 620-663, 'S', 665-771, 'R', 773
A:Cross-references: EMBL:J03889; NID:g172101; PIDN:AAA34843.1; PID:g172102
R:Morris, C.P.; Lim, F.; Wallace, J.C.
Biochem. Biophys. Res. Commun. 145, 390-396, 1987
A>Title: Yeast pyruvate carboxylase: gene isolation.
A:Reference number: S05760; MUID:87241529; PMID:3036126
A:Accession: S05760
A:Molecule type: DNA
A:Residues: 1003-1178 <MOR>
A:Cross-references: EMBL:J03889
A:Accession: A29722
A:Molecule type: protein
A:Residues: 1124-1149 <MOR2>
C:Genetics:
A:Gene: SGD:PYC1; PYV; MIPS:YGL062w
A:Cross-references: SGD:S0003030; MIPS:YGL062w
A:Map position: 7L
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bind
C:Keywords: biotin binding; gluconeogenesis; homotetramer; ligase; zinc
F:21-478/Domain: biotin carboxylase homology <BCH>
F:157-331/Domain: ATP/bicarbonate binding #status predicted <ATB1>
F:353-468/Domain: ATP/bicarbonate binding #status predicted <ATB2>
F:569-908/Domain: pyruvate binding #status predicted <PYK>
F:1096-1169/Domain: lipoyl/biotin-binding homology <LPB>
F:1135/Binding site: biotin (Lys) (covalent) #status experimental

Query Match	Best Local Similarity	Matches	Score	Pred. No.	Length	Indels	Gaps
42.4%	46.7%	541;	2457;	4	1178;	401;	16;
Conservative	173;	Mismatches	401;	Indels	44;	Gaps	16;
Qy	14	KILVANGETAVRAFRALLETGAATVAIYPREDGRSFHRSFAEVRIGTEG--SPVKAY	71				
Db	21	KILVANGETPIRIFFTHAHLSMTVAIYSHEDLSTHKOKADEAVYGVGYTPVGAY	80				
Qy	72	LDTDELIIGAKKVKADAIYPGVGFSENAQLARECAENGITTFIGTPEVLDTGDKSRAY	131				
Db	81	LAIDEIISIAQKHQVDIFHPGGVFSENSEFAKDVKGAGITWIGPPAEIVDSVGDKVSAR	140				
Qy	132	TAAKAGLVPLAEST--PSKNNDIEVKSASGQTYPIFKVAVAGGGGRMRFNVASPDRLKL	190				
Db	141	NLAAKANVTVPCTPGPIETVEALDFVNEYGPVIIRKAAGFGGGRMVVREGDDVADA	200				
Qy	191	ATEASREAAAGDGAVYVERAVINPQHLEVOILDGHTEVVHLRYERDCSLQRHQKVVE	250				
Db	201	FQRTSEARTAFNGFCFVERFLDPKHTEVOLLDADNHGNVYVHLFERDCSVQRHQKVVE	260				
Qy	251	IAPAQHLDELDRICADAVKCFRSIGYGACTVEFLVDEKGNHVFIEMNPRIQYEHVTV	310				
Db	261	VAPAKTLPREVDAILTDVAKLAKCEGYRNAGTAELFDVNQRHFIEINPRIQYEHVIT	320				
Qy	311	EEVTEVDLYQMRLAAGATLKELGLTQDKIKTHGAALQCRTTTEDPNNGFRPDTGITTA	370				

Db 321 BEITGIDIVAAQIQTAAGASLPQLGLFQDKITTRGFATQCRITTEDPAKNFQPDGTGRIEV 380
QY 371 YRSPGAGVRLDGA-AQLGGEITAHFDSMLVKMTCRGSDFFETAVARAQALAEFTVSGVA 429
Db 381 YRSAGNGVRLDGGNAYAGTIISPHYSMLVKYCSGSGTYEIVRKIMIRALIEFKIRGVK 440
QY 430 TNIGFLRALLREEDFTSKRIATGFTADHPHLLQAPPADDEQGRILDYLADEVN----KP 485
Db 441 TNIPFLLLLNPNVFIETTYWTFIDDDTPQLFQMYSSONRAQKLLHYLADVAVNGSSIKG 500
QY 486 HGVPRKDVAAPIIDKLPNIKDL-----PLPRGSRDLKQLGPAAPAFARDLREODALA 535
Db 501 QIGLPLKLSNP--SVPHLHDAGNVINVTKSAPPSGNQVLLLEKPAEFARQVRNGTL 558
QY 536 VYDTTFRDAHOSLLATRVRSFALKPAAPAVAKLTPELLSVEAWGATYDVAMRFLFEDPW 595
Db 559 LMDTTRDAHOSLLATRVTRTHLATIAPTAAHALAGREALECGGATFDVAMRFLHEDPW 618
QY 596 DRLEDELREAMPNVNOMLLRGNTVGYTPYDPSVCRAFVKEAASSGVDFIRFEDALNDVS 655
Db 619 ERRLKRLSLVNPFPQMLRGANGVAYSSLFDNAIDHFVKQAKDNGVDIFRVFDALNDLE 678
QY 656 QMRPAIDAVLETNTAVAVAMAYSGDLSDPNEKLYLDYILKMAEEIVKSGAHILAIKDM 715
Db 679 QLKVGVDVKKAG-GVVEATVCFSDMLQPGKK-YNLDIYLEIAEKIVQMGTTHILGKDM 736
QY 716 AGLRPAAVTKLVTLALREF-DLPVHVHTDAGQLATYFAAAQAGADAVDASAPLSG 774
Db 737 AGTKPAAAKLLIGSLRAKYPDLPITHVHTDSAGTAVASMTACALAGADVVDVAINMSG 796
QY 775 TTSOPSLSAIVAAFAHTRDGTLSLEAVSDLEPYWEAVRGLYLPESGTPGTGRVYRHE 834
Db 797 LTSQPSINALLASL-EGNIDTGINVEHVRELDAYAEMLLYSCFEADLKGPDPPEVYQHE 855
QY 835 IPGGQSLNRAQATVALGLADRFELLIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVGAG 894
Db 856 IPGGQTLNLLFQAQQLGGEQWAEKTRAYREANYLLGDIVKTPTSKVVGDLAQFVWSNK 915
QY 895 VDPADFAADPOKIDIPDSVIAFLRGELGNPPGGWPEPLRTRALEGRSEKAPLTVPEEE 954
Db 916 LTSDDVRLANSLDPPDSVMDFFEGILGQPYGGPPEPFRSDVLRNK---RRKLTORPGL 972
QY 955 QAHLDADDKERNLSNRL-----LFPKPTFEFLEHRRRFGNTSALDDREFFY 1002
Db 973 LEPPDLE--KIREDLQNRFGDVDECDVASYNMYPVYEDFOKMRETYGDLSVLPTRFSL 1030
QY 1003 GLVEGRETLIRLPDVRTPLLVRLDAISEPDDK-GMRNVVANVNGOIRPMVRDRSVESVT 1061
Db 1031 PLETDEETEVVEQKGT-LIILQLQAVGLNKKTGEREVYFDLNGEMRKIRVADRSQKVET 1089
QY 1062 ATAEDSSNKGHVAAPAGV-VTVVAEGDEVKAGDAVAITEAMKEPATITASVDGKID 1120
Db 1090 VTKSKADMDPLHIGAPMAGVIVEVKHKSLLIKKQPVAVLSAMKMEMIITSSPSDGOVK 1149
QY 1121 RVVYPAATKVEGDLIVVV 1139
Db 1150 EVFVSDGENVDSSDLLVLL 1168

Search completed: September 24, 2003, 16:00:32
Job time : 39.741 secs

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OM protein - protein search, using sw model

Run on: September 24, 2003, 15:44:03 ; Search time 18.3631 Seconds
(without alignments)
2919.469 Million cell updates/sec

Title: US-09-974-973A-19

Perfect score: 5788

Sequence: 1 MSTHTSTLPAFKKILVANR.....RVVPAATKVEGGDLIVVWS 1140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2541.5	43.9	1178	1 PYC_MOUSE	Q05920 mus musculus
2	2525.5	43.6	1178	1 PYC_RAT	P52873 rattus norv
3	2520.5	43.5	1178	1 PYC_HUMAN	P11498 homo sapien
4	2457	42.4	1178	1 PYC_YEAST	P11154 saccharomyc
5	2436	42.1	1180	1 PYC_YEAST	P32327 saccharomyc
6	2391	41.3	1189	1 PYC_PICPA	P78992 pichia past
7	1079	18.6	501	1 PYCA_METJA	O58626 methanococc
8	1036.5	17.9	447	1 ACCC_ANASP	O06862 anabaena sp
9	1019	17.6	506	1 PYCA_ARCFU	O30019 archaeoglob
10	997	17.2	491	1 PYCA_METTH	O27939 methanobact
11	946	16.3	448	1 ACCC_HAEIN	P43873 haemophilus
12	938	16.2	449	1 ACCC_ECOLI	P24182 escherichia
13	936	16.2	449	1 ACCC_ECO57	O8x9b6 escherichia
14	924	16.0	449	1 ACCC_PSEAE	P37798 pseudomonas
15	911	15.7	725	1 MCCA_HUMAN	O96rq3 homo sapien
16	909	15.7	717	1 MCCA_MOUSE	O99mr8 mus musculu
17	883.5	15.3	654	1 BCCA_MYCTU	P46401 mycobacteri
18	879	15.2	448	1 ACCC_BACSU	P49787 bacillus su
19	875.5	15.1	598	1 BCCA_MYCLE	P46392 mycobacteri
20	871.5	15.1	567	1 PYCB_METJA	O58628 methanococc
21	866	15.0	703	1 PCCA_HUMAN	P05165 homo sapien
22	859.5	14.8	731	1 MCCA_SOYBN	Q42777 glycine max
23	859	14.8	734	1 MCCA_ARATH	Q42523 arabidopsis
24	843.5	14.6	704	1 PCCA_RAT	P14882 rattus norv
25	835.5	14.4	1835	1 DURL_YEAST	P32528 saccharomyc
26	825	14.3	568	1 PYCB_METTH	O27179 methanobact
27	804	13.9	590	1 DCOA_SALTY	O03030 salmonella
28	799.5	13.8	595	1 DCOA_KLEPN	P13187 klebsiella
29	612.5	10.6	2345	1 COAL_RAT	P11497 rattus norv
30	609.5	10.5	2324	1 COAC_CHICK	P11029 gallus gall
31	609.5	10.5	2346	1 COAL_HUMAN	Q13085 homo sapien
32	608.5	10.5	2346	1 COAL_BOVIN	O9tts3 bos taurus
33	601	10.4	2346	1 COAL_SHEEP	Q28559 ovis aries

ALIGNMENTS

RESULT 1

ID	PYC_MOUSE	STANDARD;	PRT;	1178 AA.
AC	Q05920;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic			
DE	carboxylase) (PCB).			
GN	PC OR PCX.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Adipocyte;			
RX	MEDLINE=93189578; PubMed=8446588;			
RA	Zhang J., Xia W.L., Brew K., Ahmad F.;			
RT	"Adipose pyruvate carboxylase: amino acid sequence and domain			
RT	structure deduced from cDNA sequencing."			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:1766-1770(1993).			
CC	-1- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION			
CC	INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY			
CC	ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE			
CC	CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE			
CC	SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY)			
CC	AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.			
CC	-1- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +			
CC	oxaloacetate.			
CC	-1- COFACTOR: BIOTIN AND MANGANESE.			
CC	-1- PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS.			
CC	-1- SUBUNIT: Homotetramer.			
CC	-1- SUBCELLULAR LOCATION: Mitochondrial matrix.			
CC	-1- TISSUE SPECIFICITY: LIVER, KIDNEY, ADIPOSE TISSUE, LIVER			
CC	AND BRAIN.			
CC	-1- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES			
CC	AND CARBAMYL PHOSPHATE SYNTHETASES.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL; L09192; AAA39737.1; ..			
DR	PIR; A47255; A47255.			
DR	HSSP; P24182; IBNC.			
DR	SWISS-2DPAGE; Q05920; MOUSE.			
DR	MGI; MGI:97520; PCX.			
DR	InterPro; IPR001882; Biotin attach.			
DR	InterPro; IPR005482; Biotin carb.C.			
DR	InterPro; IPR000089; Biotin_lipoYL.			
DR	InterPro; IPR005479; CPhase_L_D2.			

Q00763 homo sapien
P32874 saccharomyc
Q00955 saccharomyc
P78820 schizosacch
O28994 archaeoglob
O27077 methanobact
Q8xa38 escherichia
P00968 escherichia
Q8dem2 vibrio vuln
Q9wz27 thermotoga
P14846 salmonella
Q97sf3 vibrio para

34 561.5 9.7 2483 1 COA2_HUMAN
35 556.5 9.6 2273 1 HFA1_YEAST
36 537.5 9.3 2233 1 COAC_YEAST
37 511 8.8 2280 1 COAC_SCHPO
38 267.5 4.6 1076 1 CARB_ARCFU
39 264 4.6 1060 1 CARB_METTH
40 255 4.4 1072 1 CARB_ECO57
41 255 4.4 1072 1 CARB_ECOLI
42 254.5 4.4 1077 1 CARB_VIBVU
43 253.5 4.4 1099 1 CARB_THEMA
44 251.5 4.3 1074 1 CARB_SALTY
45 251.5 4.3 1077 1 CARB_VIBPA

DR InterPro: IPR005481; CPhase_L_N.
 DR InterPro: IPR000891; HMGL-like.
 DR InterPro: IPR003379; PYC_OADA.
 DR InterPro: IPR005930; Pyruv_Carbox.
 DR Pfam: PF02785; Biotin_Carb.C: 1.
 DR Pfam: PF00364; biotin_lipoyl; 1.
 DR Pfam: PF00289; CPhase_L_chain; 1.
 DR Pfam: PF02786; CPhase_L_D2; 1.
 DR Pfam: PF00682; HMGL-like; 1.
 DR Pfam: PF02436; PYC_OADA; 1.
 DR TIGRFAMs: TIGR01235; pyruv_carbox; 1.
 DR PROSITE: PS00188; BIOTIN; 1.
 KW Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;
 KW ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide.
 FT TRANSIT 1 20
 FT CHAIN 21 1178
 FT DOMAIN 21 549
 FT DOMAIN 550 1000
 FT DOMAIN 1096 1178
 FT NP_BIND 198 203
 FT ACT_SITE 328 328
 FT BINDING 1144 1144
 FT SEQUENCE 1178 AA; 129684 MW; 14CEA0F9DA8B8127 CRC64;

Query Match 43.9%; Score 2541.5; DB 1; Length 1178;
 Best Local Similarity 47.0%; Pred. No. 6.7e-129;
 Matches 537; Conservative 187; Mismatches 401; Indels 17; Gaps 11;

QY 13 KKILVANRGEIAVRAFAALETGAATVAIYPREDGSRHRSFASAAVRIGTSGPVKAYL 72
 DB 38 KVMVANRGEIAIRVRACTEIGRTVAVYSQDTGQMHQKADAYLIGRLAPVQAYL 97

QY 73 DIDEIGAAKKYADAIYPCYGLFSENQAARECAENGITFGTPEVLDLGTGDKSRAYT 132
 DB 98 HIPDIIVKAVGVDAVHPGYGLSERADFAQACDAGVRFITGSPSPVVRKMGDVEARA 157

QY 133 AAKKAGLPVL-AESFSPKNIDIVSAEQGTPIPVKAVAGGGGRMRFPVAPDELKLA 191
 DB 158 IAIAGVPVPGTSPISLSHAHEFSNFGFPIIFKAAYGGGGRMRVHVHSEYEENY 217

QY 192 TEASREAAEAFGDGAVYVRAVINPOHIEVQILGDHTGWHLYERDCSLORRHOKVVEI 251
 DB 218 TRAYSEALAFNGALFVEKFEKPHIEVQILGQYGNILHYERDCSIQRHOKVVEI 277

QY 252 APAQHLDPRLDRICADAVKFORSIGYQAGTVEFLVDEKGNHVFIEMPRIQVEHTVE 311
 DB 278 APATHLDPOLRSRLTSDSVKLAKQVYENAGTVEFLVDEKGNHVFIEVNSRLQVEHTVE 337

QY 312 EYTEVDLVKAQMLAAGATLKLGLTQDKIKTHGALOCRITTEDPNNGFRPDGTITAY 371
 DB 338 EITVDLVHAQIHVSEGRSLPDLGRQENIRINGCAICQRTVEDPARSFQPDGTGRIEYV 397

QY 372 RSPGGAGVRLDGAQL-GSEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTVSGVAT 430
 DB 398 RSGEGMGIRLDNASAFQGAVISPHYDVLVKKVIAHGKHDPHTAATKMSRALAEFRVGYKT 457

QY 431 NGCFRALLREDFTSKRIATGFIADHPLHLQAPADDEQGRILYLDADTVNKHGVRP 490
 DB 458 NIPFLQNLNNOOFLAGTVDTFIDENPELFOLRPAQNRQAOKLHYLGHVWVNGTPTIP 517

QY 491 KDVA-APID-KLPNLIKDLPLPRGSRDLKOLGPAFAFDRLEQDALAVDTDFRAHOSL 548
 DB 518 VNVSPSPDPAVPVPIGPPAGFRDLLEREGPEGFARAVRNHQGLLMDTDFRAHOSL 577

QY 549 LATRVRSFALKPAAPAAVAKLTPELLSVEAWGATYDVAMRFLFEDPWRDLREAMPNV 608
 DB 578 LATRVTHDLKKIAPVVAHNFKLSMENWGATDVAMRFLYECPPWRRLQELRELINI 637

QY 609 NIQMLLRGNTVGYTPYDSCVRAVKEAASGVDFIFRIDALNDVDSQMRPAIDAVLETN 668
 DB 638 PFQMLLRGANAVGYTNYPDNVVFKFEVAKENGMDVFRVDSLNYLPNNMLLMEAGSAG 697

QY 669 TAVAEVAMAYSGDLPNEKLYTLDYLLKMAEIEIVKSGAHILAIDKDMAGLLRPAAVTKIV 728
 DB 698 -GVVEAAISYTGDAVDPSTKSYLSLEYVMGLAEELVRAAGTHILCIKDMAGLLRPAACTMLV 756

QY 729 TALRREF-DLPVHVHTHTAGQLATYFAAAGAGADAVDGCASAPLSGTTSSQSLSIYAA 787
 DB 757 SSLRDRFPDLPLHITHDTSGAGVAAMLACAAGADVVDVAVDSMSGMTSQSPSMGALVAC 816

QY 788 FAHTRDRDTGLSLEAVSDLEPPYWEAVRGLYLPTEFSGTPGPTGR--VYRHEIPGGQSLNLA 845
 DB 817 TKGTPDLDTVEPLERVDYSEYWEAGRLYAAFDCTATMKSNGSDVYENELPGGQYTNLF 876

QY 846 QATAGLADRFELIEDNYAAVNMGLRPTKVTPTSSKVGWGDIALHLVAGVDPADFAADPQ 905
 DB 877 QAHSMLGSGKFEVKAYVEANQMLGDLLIKVTPSSKIVGDLAQEFMYQVNGLSRAEAEAAQAE 936

QY 906 KYDIPDSVIAFLRGLGNLPGGWPPELRFAL-----EGRSEGRAPLIEVEEQAHL 959
 DB 937 ELSEFRSVVEFLOGYIGIPHGFPPEFNSKVLKDLIPRIEGRFGASLPPNLKLEKDLID 996

QY 960 A-DDSKERNRNLRLIFPKPTTEEFLEHRRRFGNTSALDDREFFYGLVEGRETLIRLPDVR 1018
 DB 997 RHGEVTPEDVLSAAMYPDVFAQKDFATFGPLDSLNTFLQGPKEAEFEVELEKCK 1056

QY 1019 TPLLVRDLAISPDGDKGMNVVANVNGQIRPMVRDRSVESVTATAEKADSSNKGHVAAP 1078
 DB 1057 T-LHIKALAVDLNRAGQRQVFFELNGQLRSILVKDTQAMKEMHFPKALKDKVKGQIGAP 1115

QY 1079 FAG-VVTVMVAGDEVKAGDAVAITAEAKMEATITASVDGKTDVVVPAATKVEGGDLIV 1137
 DB 1116 MFGKVIDIKVAAGDKVAKGQPLCVLSAMKREIVTVTSPMEGTRKVVHTKDMTLEGDDLIL 1175

QY 1138 VV 1139
 DB 1176 EI 1177

RESULT 2
 PYC_RAT
 ID PYC_RAT STANDARD; PRT; 1178 AA.
 AC P52873; Q64555;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic
 carboxylase) (PCB).
 GN PC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RP [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96096548; PubMed=8522203;
 RA Lehn D.A., Moran S.M., Macdonald M.J.;
 RT "The sequence of the rat pyruvate carboxylase-encoding cDNA.";
 RL Gene 165:331-332(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=96257760; PubMed=8687410;
 RA Jitrapakdee S., Booker G.W., Cassidy A.I., Wallace J.C.;
 RT "Cloning, sequencing and expression of rat liver pyruvate
 carboxylase.";
 RL Biochem. J. 316:631-637(1996).
 CC !- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
 INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
 ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE
 CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE
 SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY)
 AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.
 CC !- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +

GN PC. Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Liver;
RX MEDLINE=95002203; PubMed=7918683;
RA Wexler I.D., Du Y., Lisgaris M.V., Mandal S.K., Freytag S.O.,
RA Yang B.-S., Liu T.-C., Kwon M., Patel M.S., Kerr D.S.;
RT "Primary amino acid sequence and structure of human pyruvate
carboxylase.";
RL Biochim. Biophys. Acta 1227:46-52(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=94324922; PubMed=8048912;
RA Mackay N., Rigat B., Douglas C., Chen H.S., Robinson B.H.;
RT "cDNA cloning of human kidney pyruvate carboxylase.";
RL Biochem. Biophys. Res. Commun. 202:1009-1014(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Liver;
RX MEDLINE=94324922; PubMed=8048912;
RA Mackay N., Rigat B., Douglas C., Chen H.S., Robinson B.H.;
RT "cDNA cloning of human kidney pyruvate carboxylase.";
RL Biochem. Biophys. Res. Commun. 202:1009-1014(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1083-1178 FROM N.A.
RX MEDLINE=87212051; PubMed=3555348;
RA Lamhonwah A.-M., Quan F., Gravel R.A.;
RT "Sequence homology around the biotin-binding site of human propionyl-
CoA carboxylase and pyruvate carboxylase.";
RL Arch. Biochem. Biophys. 254:631-636(1987).
RN [6]
RP SEQUENCE OF 1135-1178 FROM N.A.
RX MEDLINE=85030380; PubMed=6548474;
RA Freytag S.O., Collier K.J.;
RT "Molecular cloning of a cDNA for human pyruvate carboxylase.
Structural relationship to other biotin-containing carboxylases and
regulation of mRNA content in differentiating preadipocytes.";
RL J. Biol. Chem. 259:12831-12837(1984).
RN [7]
RP VARIANTS PC DEFICIENCY THR-610 AND ILE-743.
RX MEDLINE=98254451; PubMed=9585612;
RA Carbone M.A., Mackay N., Ling M., Cole D.E.C., Douglas C., Rigat B.,
RA Feigenbaum A., Clarke J.T.R., Haworth J.C., Greenberg C.R.,
RA Seargeant L., Robinson B.H.;
RT "American pyruvate carboxylase deficiency is associated with two
distinct missense mutations.";

Am. J. Hum. Genet. 62:1312-1319(1998).
[8]
RL VARIANTS PC DEFICIENCY ALA-145 AND CYS-451.
RN MEDLINE=98244401; PubMed=9585002;
RX Wexler I.D., Kerr D.S., Du Y., Kaung M.M., Stephenson W., Lusk M.M.,
RA Wappner R.S., Higgins J.J.;
RT "Molecular characterization of pyruvate carboxylase deficiency in two
conanguineous families.";
RL Pediatr. Res. 43:579-584(1998).
CC -!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE
CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE
SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY)
AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.
CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
oxaloacetate.
CC -!- COFACTOR: BIOTIN AND MANGANESE.
CC -!- PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- DISEASE: Defects in PC are the cause of pyruvate carboxylase
deficiency (PC deficiency) [MIM:266150] leading to lactic
acidosis, mental retardation and death. It occurs in three forms:
CC mild or type A, severe neonatal or type B, and a very mild
CC lacticacidemia.
CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
AND CARBAMYL PHOSPHATE SYNTHETASES.
CC
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CC
CC EMBL: U04641; AAA99537.1; -;
CC EMBL: S72370; AAB31500.1; -;
CC EMBL: U30891; AAA82937.1; -;
CC EMBL: BC011617; AAH11617.1; -;
CC EMBL: M26122; AAA36423.1; -;
CC EMBL: K02282; AAA60033.1; -;
CC PIR: G01933; J02460.
CC HSP: P24182; IBNC.
CC Genew: HGNC:8636; PC.
CC GK: P11498; -;
CC MIM: 266150; -;
CC GO: GO:0005524; F:ATP binding activity; TAS.
CC GO: GO:0009374; F:biotin binding activity; TAS.
CC GO: GO:0004736; F:pyruvate carboxylase activity; TAS.
CC InterPro: IPR001882; Biotin_attach.
CC InterPro: IPR005482; Biotin_carb.C.
CC InterPro: IPR005089; Biotin_lipoyl.
CC InterPro: IPR005479; CPase_L_D2.
CC InterPro: IPR005481; CPase_L_N.
CC InterPro: IPR000891; HMGL-like.
CC InterPro: IPR003379; PYC_OADA.
CC InterPro: IPR005930; Pyruv_carbox.
CC Pfam: PF02785; Biotin_carb.C; 1.
CC Pfam: PF00364; Biotin_lipoyl; 1.
CC Pfam: PF00289; CPase_L_chain; 1.
CC Pfam: PF02786; CPase_L_D2; 1.
CC Pfam: PF00682; HMGL-like; 1.
CC Pfam: PF02436; PYC_OADA; 1.
CC TIGRFAMs: TIGR01235; pyruv_carbox; 1.
CC PROSITE: PS00188; BIOTIN; 1.
KW Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;
KW ATP-binding; Mitochondrion; Lipid synthesis; Transit peptide;
KW Disease mutation.
FT TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
FT CHAIN 21 1178 PYRUVATE CARBOXYLASE.
FT DOMAIN 21 549 BIOTIN CARBOXYLASE (BY SIMILARITY).

QY 649 DALNDYSQMPAIDAVLETTAVAEVAMAYSGDSDPNEKLYTIDYLRKMAEEIVKSGAH 708
 Db 673 DALNDLEQLKVGNAVKKAG-GVVEATVYSGDMLQPKK-YNLDYILEVEKIVQMGT 730
 QY 709 ILAKMAGLLRAAVTKLTALRREF-DLPVHVHDTAGGQAIYFAAQAQADAVDG 767
 Db 731 ILGKDMAGTFAAATKLTGSRYPDLPPIHVSHSDSAGTAVASMTACALAGADV 790
 QY 768 ASAPLSGTTSPQSLSAIYAAFAHTRDTGLSLAVSDLEPYWEAVRGLYLPFFSGTGP 827
 Db 791 AINSMGLTSPQSLNALLASL-BGNIDTGINVHRELDAYWAEMLLYSCFADLKGPD 849
 QY 828 GRYRHEIPGQSLNRAQATAGLADRFELIEDNVAANEMLRPTKVTTPSSKVGDLA 887
 Db 850 PEYQHEIPGQSLNRAQATAGLADRFELIEDNVAANEMLRPTKVTTPSSKVGDLA 909
 QY 888 LHLVAGVDPADFAADPKQKIDPDSVIAFLRGLGNPPGPGWPEPLRTRALEGSEKAPL 947
 Db 910 QFVSNKLTSDDDRRLANSILDFDSDVMDFFEGILQPGYGGFPEPLRSDVLRNK---RRKL 966
 QY 948 TEVPEEQAHLDADDKERNLSNRL-----LPPKPTFEFFLEHRRRFGNITSAL 995
 Db 967 TCRPGLLEPFDE--KIREDLQNRFGDIDECOVASVNMYPVRYEDFQKIRETYGDL 1024
 QY 996 DDEFFYGLVEGRETILRLPDRVTPILVRLDAISEPDDK-GMRNVVANVNGQIRPMKVRD 1054
 Db 1025 PTNKLAPAEDEIEVTEIQGKT-LIIRKQAVGDLNKKTGQREVYFELNGELRKIRVAD 1083
 QY 1055 RSVESYATAEKADSSNKGHVAAPFAGV-VTVTVAEGDEVKAGDAVAITFAMKEATITA 1113
 Db 1084 KSONIQSVAKPKADVHTQIGAPMAGVIEVKHGLSVKKGESTAVLSAMKEMWVSS 1143
 QY 1114 SVDGKIDRVVPAATKVEGDLVVV 1139
 Db 1144 PADGVKDFIKDGSVDASDLVL 1169

RESULT 6

PYC_PICPA STANDARD; PRT: 1189 AA.
 AC P/8992;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Pyruvate carboxylase (EC 6.4.1.1) (pyruvic carboxylase) (PCB).
 GN PYC1.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID=4922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98301182; PubMed=9639311;
 RA Menendez J., Delgado J., Gancedo C.;
 RT "Isolation of the Pichia pastoris PYC1 gene encoding pyruvate
 RT carboxylase and identification of a suppressor of the pyc
 RT phenotype".
 RL Yeast 14:647-654(1998).
 CC -!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
 CC INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
 CC ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE
 CC CARBOXYL GROUP TO PYRUVATE IN THE SECOND (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
 CC oxaloacetate.
 CC -!- COFACTOR: BIOTIN AND ZINC.
 CC -!- PATHWAY: Gluconeogenesis.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
 CC AND CARBAMYL PHOSPHATE SYNTHETASES.
 CC -----

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 CC or send an email to license@isb-sib.ch.
 CC -----

CC EMBL; Y11106; CAA71993.1; --
 DR HSPP; P24182; IDV1.
 DR InterPro; IPR001882; Biotin_attach.
 DR InterPro; IPR005482; Biotin_carb_C.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR InterPro; IPR005483; Cphase_L.
 DR InterPro; IPR005479; Cphase_L_D2.
 DR InterPro; IPR005481; Cphase_L_N.
 DR InterPro; IPR000891; HMGU-like.
 DR InterPro; IPR003373; PYC_OADA.
 DR InterPro; IPR005930; Pyruv_carbox.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF00364; biotin_lipoyl; 1.
 DR Pfam; PF00289; Cphase_L_chain; 1.
 DR Pfam; PF02786; Cphase_L_D2; 1.
 DR Pfam; PF00682; HMGU-like; 1.
 DR Pfam; PF02436; PYC_OADA; 1.
 DR PRINTS; PR00096; CPSASE.
 DR TIGRfams; TIGR01235; pyruv_carbox; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 DR PROSITE; PS00866; CPSASE_1; 1.
 DR PROSITE; PS00867; CPSASE_2; 1.
 KW Ligase; Multifunctional enzyme; Biotin; Gluconeogenesis; ATP-binding;
 KW Zinc.
 FT NP_BIND 185 190 ATP (POTENTIAL).
 FT ACT_SITE 315 315 BY SIMILARITY.
 FT BINDING 1140 1140 BIOTIN (BY SIMILARITY).
 FT SEQUENCE 1189 AA; 131400 MW; 856E858079657914 CRC64;

Query Match 41.3%; Score 2391; DB 1; Length 1189;
 Best Local Similarity 45.3%; Pred. No. 8.2e-121;
 Matches 526; Conservative 177; Mismatches 423; Indels 34; Gaps 16;
 QY 6 SSTLPAPFKILVANRGEIAVRAFAALETGAATVAIVPREDGRSPHSFASAVRIGTEG 65
 Db 16 SLLGTMTNKLIVANRGEIPIRPTAHLSMTVAIVSHEDRLSMRLKADEAYVIGERG 75
 QY 66 --SPVKAYLDIDIEIGAAKKVADAIYPGYGLSENAQLARECAENGITFIGPTPEVLDL 123
 Db 76 QYSPVQAYLAIDIEIKIAVKNNVMTHPGVGFCSENSEFARKVEENGILWVGSDAVIDA 135
 QY 124 TGDKSRVTAAKKAGLPVLAEST-PSKNIDEIVKSAEGOTYPIFYKAVAGGGGRMFVA 182
 Db 136 VGDKVSARNLVAANVTVPPTGPIEDVAQATAFVEEYGYPIVTKAAGGGGRMRVVR 195
 QY 183 SPDELKRLATEASREAAAFGDAVYVERAVINPQHIEVQILGDHTGEVYVHLVYERDCSQ 242
 Db 196 EGGDIEDAFLRASSEAKTAFNGTVPFIERFLOKPKHIEVQLLADNAGNVVHLFERDCSVQ 255
 QY 243 RHQKVEIAPAHQLDPELDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFTEMNPR 302
 Db 256 RHQKVARNCASAKTLFPEVVRNAILNDVAKLAKTANYRNAGTAEFVLDVSDNRHYFEINPR 315
 QY 303 IOVEHVTVEEVDVLVKAQMLAAGATLKLGLTQDKLTKHGAALOCITTEDENNGFR 362
 Db 316 IOVEHITTEITGVDIVAAQIOIQAAGASLEQLGLQEKITTTGFAIQCRITTEDPTKNFQ 375
 QY 363 PDTGITAYRSPGGAGVRLDGAALGGE-ITAHFDSMLVKMTCRGSDFETAVARAQALA 421
 Db 376 PDTGKIEVYRSSGGNGVRLDGGNGFAGAVISPHYDSMLVKCSTSGSNVEIRRKMLRALV 435
 QY 422 EFTVSGVATNIGFLRALLREEDFTSKRTATGFIADPHLLQAPDADDEGRILDIADVT 481
 Db 436 EFERIGVKTNPFLPALLTHPVFMTSECVTTTIDTPELTKILTSONRAKQLLAVLGDLA 495
 QY 482 VN-----KPHGVKPKDVAAPIDKLPIKID--LPLPRGSRDLKQLGPAFARDL 528

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Db 496 VNGSSIKGQIGLPLKH--KEADIPSTIDINGVIDVSIPLPPDGRWROFLLEKKGPEQPAQV 553
QY 529 REQDALAVDTTTPRDAHQSLATRVRSFALKPAEAAVAKLTPELLSVEMGGATYDVAMR 588
Db 554 RAFPGLIMDTWRDHAQSLATRVTRTHLLNIAPATSYALHHAFALECGWGGATFDVSMR 613
QY 589 FLFEDPWRLDELREAMPNNIOMLLGRNTGYTYPDSVCRFAFKVKEAASSGVDFRIF 648
Db 614 FLHEDPWRLKLRKAVNPFPFSLRGGNGVAYISLPDNIADHFLKQAKDTGVDFRIF 673
QY 649 DALNDVSRMPADAYLEINTAEVAMAYSGDLSDPNEKLYLDYLLKMAEIVKSGAH 708
Db 674 DALNDIEQLKGVDAVKKAG-GVVEATMCSGMDLPKPK-KYNEIYINLAIIEVEMGH 731
QY 709 ILAIKDMAGLLPRAVTKLVLTALRREF-DLPVHVHPTDAGQOLATYFAAQAQADAVDG 767
Db 732 ILAVKDMAGTLKPTAKOALISALRRKFPSPHIVHPTDAGTGVASWACARAGADVTV 791
QY 768 ASAPLSGTTSPQSLSAIVAAFAHTRDGTGLSLEAVSDLEPYNEAVRGLYLPESGTPGPT 827
Db 792 RYNSMGMTSPQSMASFIASL-DGEIETGIPANAREIDAYWAEMLLYSCFEADLKGP 850
QY 828 GRVYRHEIPGGQSLNRAQATGALADREFELIEDNYAAVNEMLGRPTKVPSSKVVGDIA 887
Db 851 PEVYQHEIPGGQTLNLLFQAQVGLKEKWKVETKKAYEAAANRLLDIVKVTPTSKVVGDIA 910
QY 888 LHLVAGVDPADFAADPKYDIPDSVIAFLRGLGNPPGWPPELRTALRGRSE---GK 944
Db 911 QFVNSKUSSEVERLASELDPFSDVDFEGLMGTYPGGFPEPLRTNVISGKRRLTSR 970
QY 945 APLTEVPEBEQA---HL0ADDSKERNSL-NLLLPKPTPEEFLERHRRFGNTSALDDREF 1000
Db 971 PGLTLEPNIPAIREDLEARFSKVTENDVASVNMYPKYVEAKKQOELGDLISVLPTNRF 1030
QY 1001 FY-GLIVEGREPLRLDVPRTPLLVRLDAISE-PDDKGMNVVAVNVNGQIRPMRYDRSV 1057
Db 1031 LSPPKIDEERHVTIYTIETKTLIIKCAEGELSSQSGTREVYFELNGEMRKVTYEDKNG 1090
QY 1058 ESVTATAKADSNKGHVAAAPAGVVT-VTVAGDEVKAGDAVAIIKAMKEATTASVD 1116
Db 1091 AVETTRKADAHNNEIGAPMAGVVVEVRHENGVEVKKGDPPIAVLSAMKMEMVSSPYA 1150
QY 1117 GKIDRVVPAATKVEGGDLI 1136
Db 1151 GRIGQIAVKENDSVDAASDLI 1170

RESULT 7
PYCA_METJA
ID PYCA_METJA STANDARD; PRT; 501 AA.
AC Q58626;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic carboxylase A).
GN PYCA OR M1229.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kierulff A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus

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RT jannaschii.";
RL Science 273:1058-1073(1996).
RN [2]
RP SEQUENCE OF 1-12, AND FUNCTION.
RX MEDLINE=21034791; PubMed=11195096;
RA Mukhopadhyay B., Patel V.J., Wolfe R.S.;
RT "A stable archaeal pyruvate carboxylase from the hyperthermophile
RT Methanococcus jannaschii."
RL Arch. Microbiol. 174:406-414(2000).
CC -1- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
CC INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
CC ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL
CC GROUP TO PYRUVATE IN THE SECOND.
CC -1- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-)= ADP + phosphate +
CC oxaloacetate.
CC -1- COFACTOR: ATP, MAGNESIUM (OR MANGANESE OR COBALT), PYRUVATE AND
CC BICARBONATE.
CC -1- ENZYME REGULATION: INHIBITED BY MAGNESIUM, WHEN ITS CONCENTRATION
CC EXCEEDED THE ATP ONE, AND BY HIGH CONCENTRATION OF ATP AND ALPHA-
CC KETOGLUTARATE.
CC -1- PATHWAY: Gluconeogenesis.
CC -1- SUBUNIT: HETEROOTAMER OF FOUR A AND FOUR B SUBUNITS.
CC -1- MASS SPECTROMETRY: MW=55500; METHOD=WALDI.
CC -1- MISCELLANEOUS: ITS OPTIMUM PH IS 8.5 AND THE OPTIMUM TEMPERATURE
CC IS 80-90 DEGREES CELSIUS.
CC -1- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPONAMIDE TRANSFERASES
CC AND CARBAMYL PHOSPHATE SYNTHETASES.
CC -----
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CC -----
EMBL: U67563; AB999232.1; -
DR PIR: D64453; D64453.
DR HSP: P24182; LBNC.
DR TIGR: M1229; -
DR InterPro: IPR004549; ACCC.
DR InterPro: IPR005482; Biotin_carb_C.
DR InterPro: IPR005483; CPase_L.
DR InterPro: IPR005479; CPase_L_D2.
DR InterPro: IPR005481; CPase_L_N.
DR Pfam: PF02785; Biotin_carb_C; 1.
DR Pfam: PF00289; CPase_L_chain; 1.
DR Pfam: PF02786; CPase_L_D2; 1.
DR PRINTS: PR00098; CPASE.
DR TIGRFAMs: TIGR00514; accc; 1.
DR PROSITE: PS00866; CPASE.1; 1.
DR PROSITE: PS00867; CPASE.2; 1.
KW Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
KW ATP-binding; Complete proteome.
FT NP_BIND 162 167 ATP (POTENTIAL).
FT ACT_SITE 291 291 POTENTIAL.
SQ SEQUENCE 501 AA; 55402 MW; 04D2E401892F872F CRC64;

Query Match 18.6%; Score 1079; DB 1; Length 501;
Best Local Similarity 48.2%; Pred. No. 7e-51;
Matches 218; Conservative 82; Mismatches 146; Indels 6; Gaps 4;

QY 12 FKKILVANRGEIAYRAFAALETGAATVATYIPREDGRSFHRSFASEAVRIGTEGSPVKAY 71
Db 2 FNKVLINRGEIATRIIRACWELGKIVAVVSEADKRSLSLATLADAYCIG-PAPAASKY 60
QY 72 LDIDEILGAKKVADAIYPOYGFSLNQAARCAENGITFGTPEVLDLTGDKGRAV 131
Db 61 LNDIAILNVAEKAKVDIAHPGYGLAENAEFAFARAVKAGFEFICPNPDATAMGSKINAK 120
QY 132 TAACKAGLPVLAESTPS-KNIDEIVKSAEGQTPIFYKAVAGGGGGRMRFVASDELRKL 190
Db 121 KIMKAGVLIIPGSEGAIEDIAETAEIAGFPVVVVKASAGGGGGMGMSVAYSKEELKEY 180

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QY 191 ATEASREAAFGDGAIVYVERAVINPQHTEVQILGDTGEVHLYEDRCSLQRRHQKVE 250
 Db 181 IESARNIAKSAFGDPTVFIEKYLENPRHIEQLGDKHGNIHLGDRCSLQRRHQKLE 240
 QY 251 IAPAQHLDELDRICADAVKFCRSIGYOCAGTVFELVDEKGNHVFIEENPRIQVEHTVT 310
 Db 241 EASPTWTELPRMGEAKKAGKAINYSAGVVEELY-ENGNYFLENNTRIQVEHTVT 299
 QY 311 EEVTEVDLVKAQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNNFRDPTGTITTA 370
 Db 300 EQVTGIDLVKAMIKIAAG---BELTLKQEDVKIRGHAIECRINAEDPLNDFVPCPKIKL 356
 QY 371 YRSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDEETAVARAQALAEFTVSGVAT 430
 Db 357 YRSPGPGVRIDSGVYGGAEIPYDYSMAKLIITYGNSREEARMKRALREYVIIGVKT 416
 QY 431 NIGFLRALLREEDFTSKRIATGFIADPHLIQ 462
 Db 417 NIPFHRVLEENFLKGNISTHYVEQNMKLR 448

RESULT 8

ACCC_ANASP STANDARD; PRT; 447 AA.
 AC Q06862;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA
 carboxylase) (EC 6.4.1.2) (ACC).
 GN ACC OR ALR0939.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=93352435; PubMed=8102363;
 RA Gornicki P., Scappino L.A., Haselkorn R.;
 RT "Genes for two subunits of acetyl coenzyme A carboxylase of Anabaena
 sp. strain PCC 7120: biotin carboxylase and biotin carboxyl
 carrier protein.";
 RL J. Bacteriol. 175:5268-5272(1993).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpou S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 CC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
 CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE
 CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE
 TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA.
 CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)
 = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
 CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.
 CC -!- SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN
 CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS
 OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX.
 CC -!- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-
 PHOSPHATE SYNTHETASES.

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CC EMBL; L14862; AAB51770.1; -
 DR EMBL; AF003584; BAB72896.1; -
 DR PIR; A53311; A53311.
 DR PIR; AH1923; AH1923.
 DR HSSP; P24182; LBNC.
 DR InterPro; IPR004549; AccC.
 DR InterPro; IPR005482; Biotin_carb_C.
 DR InterPro; IPR005479; Cbase_LD2.
 DR InterPro; IPR005481; Cbase_LN.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF02786; Cbase_LD2; 1.
 DR TIGRFAMS; TIGR00514; accC; 1.
 DR PROSITE; PS00866; Cbase_1; 1.
 DR PROSITE; PS00867; Cbase_2; 1.
 KW Fatty acid biosynthesis; Ligase; Biotin; ATP-binding;
 KW Complete proteome.
 FT NP_BIND 163 168 ATP (BY SIMILARITY).
 FT ACT_SITE 293 293 BY SIMILARITY.
 SQ SEQUENCE 447 AA; 49104 MW; 8A541B38B39E00F9 CRC64;

Query Match 17.9%; Score 1036.5; DB 1; Length 447;
 Best Local Similarity 48.4%; Pred. No. 1.1e-48;
 Matches 216; Conservative 73; Mismatches 152; Indels 5; Gaps 3;
 QY 12 EKKILVANGETAVRAAETGATVAIYREDGSPHRSFASAEVRICTEGSPVKAY 71
 Db 3 FDKLIANGETALRIILACEEMGIATIAVSTVDNRNALHVLQDAEAVCIG-EPASAKSY 61
 QY 72 LDIDEIIGAARKVKADAIYPGYGFLSENQAQLECAENGITITGTPPEVLDLTGDKSRV 131
 Db 62 LNIPLIAALTRNASAIHPGYGFLSENKAFKADHIAFIGTPPEAIRLWMDKSTAK 121
 QY 132 TAAKAGLPVLAESTPSKNID-EIVKSAEGQYPIPVKAVAGGGRGMFVASPDELRL 190
 Db 122 ETMQKAGVTPVPGSEGLVETEQEGLELAKDICYPMIKATAGGGGRGMFVASPDEFVK 181
 QY 191 ATEASREAAFGDGAIVYVERAVINPQHTEVQILGDTGEVHLYEDRCSLQRRHQKVE 250
 Db 182 FLAAGEGAGAGNAGVIEKFIERPHIEFOILLADNYGNVTHLGERCSIQRRNOKLLE 241
 QY 251 IAPAOHLDELDRICADAVKFCRSIGYOCAGTVFELVDEKGNHVFIEENPRIQVEHTVT 310
 Db 242 EAPSPALDSDLREKMGQAQAAQAFINVTGACTIEFLDORSQGFVEMEMNTRIQVEHPT 301
 QY 311 EEVTEVDLVKAQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNNFRDPTGTITTA 370
 Db 302 EMVTGVDLLVEQIRIAQGERLUR---LTQDVVYLGRHAIECRINAEDPDHDFRPAFGRI 358
 QY 371 YRSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDEETAVARAQALAEFTVSGVAT 430
 Db 359 YLPPGPGVRIDSHVYTDYQIPPYDLSLIGKLIWGPDRATINEMKRALRECAITGLPT 418
 QY 431 NIGFLRALLREEDFTSKRIATGFIAD 456
 Db 419 TIGFQRIMENPQFLQGNVSTSFVQE 444

RESULT 9

PYCA_ARCFU
 ID PYCA_ARCFU STANDARD; PRT; 506 AA.
 AC O30019;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic carboxylase A).
 GN PYCA OR AF0220.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;

RP SEQUENCE FROM N.A.
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Winn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriades N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.J., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Goynne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon *Archaeoglobus fulgidus*.";
 RL Nature 390:364-370(1997).
 CC -!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
 CC INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
 CC ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL
 CC GROUP TO PYRUVATE IN THE SECOND.
 CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
 CC oxaloacetate.
 CC -!- COFACTOR: ATP, MAGNESIUM (OR MANGANESE OR COBALT), PYRUVATE AND
 CC BICARBONATE (BY SIMILARITY).
 CC -!- PATHWAY: Gluconeogenesis.
 CC -!- SUBUNIT: HETEROCTAMER OF FOUR A AND FOUR B SUBUNITS (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
 CC AND CARBAMYL PHOSPHATE SYNTHETASES.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: A5001090; AAB91012.1; -
 CC PIR: D69277; D69277.
 CC DR HSP: P24182; 1BNC.
 CC DR TIGR: AF0220; -
 CC DR InterPro: IPR004549; AccC.
 CC DR InterPro: IPR005482; Biotin_carb_C.
 CC DR InterPro: IPR005479; Cpsase_L_D2.
 CC DR InterPro: IPR005481; Cpsase_L_N.
 CC DR Pfam: PF02785; Biotin_carb_C; 1.
 CC DR Pfam: PF02789; Cpsase_L_chain; 1.
 CC DR Pfam: PF02786; Cpsase_L_D2; 1.
 CC DR TIGRFAMs: TIGR00514; accC; 1.
 CC DR PROSITE: PS00866; CPSASE_1; 1.
 CC DR PROSITE: PS00867; CPSASE_2; FALSE NEG
 CC KW Ligase; Multifunctional enzyme; Gluconeogenesis; Magnesium; Pyruvate;
 CC ATP-binding; Complete proteome.
 CC FT NP_BIND 161 166 ATP (POTENTIAL).
 CC FT ACT_SITE 290 290 POTENTIAL.
 CC SQ SEQUENCE 506 AA; 57438 MW; 39B765F319235AD1 CRC64;
 Query Match 17.6%; Score 1019; DB 1; Length 506;
 Best Local Similarity 47.9%; Pred. No. 1.2e-47;
 Matches 213; Conservative 73; Mismatches 153; Indels 6; Gaps 4;
 QY 12 FKKILVNRGEIIVRAFRALAEATGAATVAIYPRDGRGSHFRSEAVRIGEGSPVKAY 71
 Db 2 FSKILVNRGEIIVRAFRALAEATGAATVAIYPRDGRGSHFRSEAVRIGEGSPVKAY 60
 QY 72 LDIDELIIGAAKKVADATPGVGFVSENAQLARCAENGITFTGPTPEVLDTGDKSRV 131
 Db 61 LNDIRIEIVAKSGAEIHPGVGFVLAENAEFAERCEEGIVFGSPVIRIAGSKVSR 120
 QY 132 TAAKAGLPLVAESTPSNIDIVKSGQYPIPVKAVAGGGGRMRFVSPDELKLA 191

Db 121 ESMORAGVPVTPGSPKIDTDEAKWEAKIGYPVAVKASGGGGIGIVVNSQELBEAF 180
 QY 192 TEASREAAFGDGAAGVYVERAVINPOHIEVOILGDHTGEVVLHYERDCSLQRHOKVVEI 251
 Db 181 RSKKLGSYFKDSTVLEKYLAPRHEIQLADQHGNIHLGERECSTQRHOKLIEE 240
 QY 252 AQAQHLDPFLDRICADAVFCRSIGYOGAGTVFELVDEKGNHVFIEIMPRIQVHTVTE 311
 Db 241 APSPALNEEREELGKLVKAGAREIGYTNAGTEFFLY-ENGNFYFLEINSRLOVEHITE 299
 QY 312 EVTEVDLVKAQMRMLAAGATLKLGLTODKIKTHGAALQCRITTEDPNNRFPDGTITAY 371
 Db 300 VVGIDIVKYQIRIAYG---EELRHGQEDVAIRGHATECRINADPPVN-FYPRSGRLHY 355
 QY 372 RSPGGAGVRDLGAAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTVSGVATN 431
 Db 356 RSPGGIGIRVDSGIHGYRIPEEYDSMISKLIAVGETREAIARMAKRLAYEIEGVETN 415
 QY 432 IGLRLALLREEDTTSKRITAGFTIAD 456
 Db 416 IPFHFAVLNDEEFVRGNHITKFEVE 440
 RESULT 10
 PYCA_METH
 ID PYCA_METH STANDARD; PRT; 491 AA.
 AC 027939;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyruvate carboxylase subunit A (EC 6.4.1.1) (Pyruvic carboxylase A).
 GN PYCA OR MTH1917.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RP SEQUENCE FROM N.A.
 RC STRAIN-Delta H;
 RC MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of *Methanobacterium thermoautotrophicum*
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-17.
 RC STRAIN-Delta H;
 RC MEDLINE=98148063; PubMed=9478969;
 RA Mukhopadhyay B., Stoddard S.F., Wolfe R.S.;
 RT "Purification, regulation, and molecular and biochemical
 RT characterization of pyruvate carboxylase from *Methanobacterium*
 RT thermoautotrophicum strain deltaH.";
 RL J. Biol. Chem. 273:5155-5166(1998).
 CC -!- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
 CC INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
 CC ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE CARBOXYL
 CC GROUP TO PYRUVATE IN THE SECOND. THE MAXIMUM ACTIVITY IS AT PH 8
 CC AND 60 DEGREES CELSIUS.
 CC -!- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
 CC oxaloacetate.
 CC -!- COFACTOR: ATP, MAGNESIUM (OR MANGANESE OR COBALT), PYRUVATE AND
 CC BICARBONATE.
 CC -!- ENZYME REGULATION: INHIBITED BY ADP AND ALPHA-KETOGLUTARATE.
 CC -!- PATHWAY: Gluconeogenesis.
 CC -!- SUBUNIT: HETEROCTAMER OF FOUR A AND FOUR B SUBUNITS.
 CC -!- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES

CC AND CARBAMYL PHOSPHATE SYNTHETASES.

CC -----

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CC -----

CC EMBL: AE000942; AAB86377.1; -

CC PIR: A69123; A69123.

CC HSSP: P24182; 1BNC.

CC InterPro: IPR004549; AccC.

CC InterPro: IPR005482; Biotin_carb_C.

CC InterPro: IPR005479; Cphase_L_D2.

CC InterPro: IPR005481; Cphase_L_N.

CC Pfam: PF02785; Biotin_carb_C; 1.

CC Pfam: PF020289; Biotin_carb_C; 1.

CC Pfam: PF02786; Cphase_L_chain; 1.

CC TIGR: TIGR00514; accC; 1.

CC PROSITE: PS00866; Cphase_1; 1.

CC PROSITE: PS00867; Cphase_2; 1.

CC Ligase; Multifunctional enzyme; Glucanogenesis; Magnesium; Pyruvate;

CC ATP-binding; Complete proteome.

CC NP_BIND 162 167

CC ACT_SITE 291 291

CC POTENTIAL.

CC SEQUENCE 491 AA; 54656 MW; 5789C34DA7475C2E CRC64;

CC -----

CC Query Match 17.2%; Score 997; DB 1; Length 491;

CC Best Local Similarity 45.9%; Pred. No. 1.7e-46;

CC Matches 205; Conservative 79; Mismatches 157; Indels 6; Gaps 4;

CC -----

CC 12 FKKILVANRGEIAVRAFAALETGAATVAIYPRDGRGFSFASAEVRIQTEGSPVKAY 71

CC 2 FSKILVANRGEIAVRAFAALETGAATVAIYPRDGRGFSFASAEVRIQTEGSPVKAY 60

CC 72 LDIDEIIGAAKKVADAIYPGFISENQAQARECAENGITFPTPEVLDITGDKSRAY 131

CC 61 LRIDRILEVAEKAGAEALHPGFGFLAENPRGEECEKOGIKLIGPKGSVIEAMGDKITSK 120

CC 132 TAAKAGLFLVAESTPS-KNIDEIVKSAEGQTPFIVKAVAGGGGGRGMRVFASPDRLRL 190

CC 121 KLMKAGVGVIPGTQGVSDPDEARAIADSGYPIVIRKASGGGIGIRAVVEEDELIRA 180

CC 191 ATEASREAEAFDGAIVYERAVINQPHIEVQILGDHTGEVYHYERDCSLQRRHOKVYE 250

CC 181 MESTQSVASAFGDPTVYIEKYLPRHIEFQVMADESGNVHLADRECSIQRRHOKLIE 240

CC 251 IAPACHLDPRLDRICADAVKFCRSGYGGAGTVEFLYDEKGNHVFIEMNRIQVEHVT 310

CC 241 EAPSPIMTPELRMGSAVAAEYIGYENAGTVEFLY-SNGDFFYLEMTRIQVEHPT 299

CC 311 EEVTEVDLVKQMLAAGATLKEGLTQDKTKTHGAALQCRITTEDPNNRFPOTGTITA 370

CC 300 EVITGVDLVKEQIRVASG---EELRFTQKDNIRNGHAEICRINAENPLADPAPNGKITG 356

CC 371 YRSPGAGVRLDGAALQGEITAFHDSMLVMTKRGSGDFEFVAVAPARALAEFTVSGVAT 430

CC 357 YRSPGAGVRLDGAALQGEITAFHDSMLVMTKRGSGDFEFVAVAPARALAEFTVSGVAT 416

CC 431 NIGFLRALLREEDFTSKRIATGFIADH 457

CC 417 TIPFHAKMNRNEAFRGELHFTFVDEY 443

CC -----

CC RESULT 11

CC ACCC_HAEIN STANDARD; PRT; 448 AA.

CC AC P43873;

CC DT 01-NOV-1995 (Rel. 32, Created)

CC DT 01-NOV-1995 (Rel. 32, Last sequence update)

CC DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA

DE carboxylase) (EC 6.4.1.2) (ACC).

GN ACCC OR HI0972.

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OC Pasteurellaceae; Haemophilus.

OX NCBI_TaxID=727;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Rd / KW20 / ATCC 51907;

RX MEDLINE=95350630; PubMed=7542800;

RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

RA Fine L.D., Fritchman J.L., Fuhmann J.L., Geoghagen N.S.M.,

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

RA Venter J.C.;

RT "Whole-genome random sequencing and assembly of Haemophilus influenzae

RT Rd.";

RL Science 269:496-512(1995).

CC -!- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A

CC CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE

CC CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE

CC TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-CoA (BY SIMILARITY).

CC -!- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)

CC => ADP + phosphate + carboxybiotin-carboxyl-carrier protein.

CC -!- PATHWAY: Long-chain fatty acid biosynthesis; first step.

CC -!- SUBUNIT: ACETYL-CoA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN

CC CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS

CC OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (BY SIMILARITY).

CC -!- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-

CC PHOSPHATE SYNTHETASES.

CC -----

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CC -----

CC EMBL: U32778; AAC22632.1; -

CC PIR: F64105; F64105.

CC HSSP: P24182; 1BNC.

CC TIGR: HI0972; -

CC InterPro: IPR004549; AccC.

CC InterPro: IPR005482; Biotin_carb_C.

CC InterPro: IPR005479; Cphase_L_D2.

CC InterPro: IPR005481; Cphase_L_N.

CC Pfam: PF02785; Biotin_carb_C; 1.

CC Pfam: PF020289; Biotin_carb_C; 1.

CC Pfam: PF02786; Cphase_L_chain; 1.

CC TIGR: TIGR00514; accC; 1.

CC PROSITE: PS00866; Cphase_1; 1.

CC PROSITE: PS00867; Cphase_2; 1.

CC Fatty acid biosynthesis; Ligase; Biotin; ATP-binding;

CC Complete proteome.

CC NP_BIND 163 168

CC ACT_SITE 292 292

CC POTENTIAL.

CC SEQUENCE 448 AA; 49108 MW; 2B497E2A31ED96D1 CRC64;

CC -----

CC Query Match 16.3%; Score 946; DB 1; Length 448;

CC Best Local Similarity 47.6%; Pred. No. 8.3e-44;

CC Matches 208; Conservative 61; Mismatches 154; Indels 14; Gaps 7;

CC -----

CC 13 KKLIVANRGEIAVRAFAALETGAATVAIYPRDGRGFSFASAEVRIQTEGSPVKAY 72

CC 3 EKVIVANRGEIAVRAFAALETGAATVAIYPRDGRGFSFASAEVRIQTEGSPVKAY 61

CC 73 DIDEIIGAAKKVADAIYPGFISENQAQARECAENGITFPTPEVLDITGDKSRAY 132

Db 62 NIPALIAAEVTVGADAIHPGYGLFLENADFAEQVERSGFTTIGPTADVIRLMGDKVSALK 121
 QY 133 AAKKAGLPVL--AESTPSKNIIDEIVKSAEGQYPIPVKAVAGSGGGRMFVAPSPDLRLK 190
 Db 122 AMKKAGVCPVSGDPVNDIAKNEIAKRIKGYPIIIKASGGGGGGRMKVRSEDALES 181
 QY 191 ATEASREARPGDGAIVYVERAVINPQHLEVOILGDHTGEVVHLYERDCSLQRHKKVVE 250
 Db 192 IAMTKAEAKAFAENDMVMEKYLENPRHVEIQVLADTHGNNAVYLAERDCSMQRHKKVVE 241
 QY 251 TAPACHLDPRLDRI--CADAVKFCRSIGYGAGTGFELVDKGNHVFIEPNRIQVEH 307
 Db 242 EAPACITTEVRDIGSRCANA--CVEIGYRGAGTFFELY-ENGFEYFIEMNTRIQVEH 297
 QY 308 TVTEEVTEVDLVKAQMLAAAGATLKGELGTQDKIKTHGAALOCRIITDPNNGRPRDGT 367
 Db 298 PVTEMITGVOLVKEQLRTAAGL---PIFKQEDIKVKGHAMECRINAEDPKT-FLPSPGK 353
 QY 368 ITAYRSPGAGVRLDGAQLGGEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTVSG 427
 Db 354 VNHLSPGGLGVWRWDVSHVYGGYVPPHYDMSIAKLITYGDTREVAIRRMQNALSETIIDG 413
 QY 428 VATNIGFELRLLEEDF 444
 Db 414 IKTNIPLHELILEDNF 430

RESULT 12

ACCC_ECOLI
 ID ACCC_ECOLI STANDARD; PRT; 449 AA.
 AC P24182;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA
 DE carboxylase) (EC 6.4.1.2) (ACC).
 GN ACC OR FRAG OR B3256.
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=K12;
 RX MEDLINE=92052166; PubMed=1682920;
 RA Kondo H., Shiratsuchi K., Yoshimoto T., Masuda T., Kitazono A.,
 RA Tsuru D., Anai M., Sekiguchi M., Tanabe T.
 RT "Acetyl-CoA carboxylase from Escherichia coli: gene organization and
 RT nucleotide sequence of the biotin carboxylase subunit."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9730-9733(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92112819; PubMed=1370469;
 RA Li S.-J., Cronan J.E. Jr.
 RT "The gene encoding the biotin carboxylase subunit of Escherichia coli
 RT acetyl-CoA carboxylase."
 RL J. Biol. Chem. 267:855-863(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX Best E.A., Knauf V.C.;
 RA Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregory J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 RN [5]

RP SEQUENCE OF 1-12.
 RC STRAIN=K12 / EMG2;
 RX MEDLINE=97443975; PubMed=9298646;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 RT in the genome of Escherichia coli K-12."
 RL Electrophoresis 18:1259-1313(1997).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE=94347758; PubMed=7915138;
 RA Waldrop G.L., Rayment I., Holden H.M.;
 RT "Three-dimensional structure of the biotin carboxylase subunit of
 RT acetyl-CoA carboxylase."
 RL Biochemistry 33:10249-10256(1994).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=20283656; PubMed=10821865;
 RA Thoden J.B., Blanchard C.Z., Holden H.M., Waldrop G.L.;
 RT "Movement of the biotin carboxylase B-domain as a result of ATP
 RT binding."
 RL J. Biol. Chem. 275:16183-16190(2000).
 CC !- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
 CC CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE
 CC CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE
 CC TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA.
 CC !- CATALYTIC ACTIVITY: ATP + biotin-carboxyl-carrier protein + CO(2)
 CC = ADP + phosphate + carboxybiotin-carboxyl-carrier protein.
 CC !- PATHWAY: Long-chain fatty acid biosynthesis; first step.
 CC !- SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHOMER OF BIOTIN
 CC CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS
 CC OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX.
 CC !- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-
 CC PHOSPHATE SYNTHETASES.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL; M79446; AAA23748.1; -
 CC EMBL; M80458; AAA23409.1; -
 CC EMBL; M83198; AAA23746.1; -
 CC EMBL; U18997; AAA58059.1; -
 CC EMBL; AE000404; AAC76288.1; -
 CC PIR; J50632; JS0632.
 CC PDB; 1BNC; 30-AUG-95.
 CC PDB; 1DV1; 09-JUN-00.
 CC PDB; 1DV2; 09-JUN-00.
 CC PDB; 1K69; 05-DEC-01.
 CC EcoGene; EG10276; accC.
 CC InterPro; IPR004549; AccC.
 CC InterPro; IPR005482; Biotin_carb_C.
 CC InterPro; IPR005479; CPase_L_D2.
 CC InterPro; IPR005481; CPase_L_N.
 CC Pfam; PF02785; Biotin_carb_C; 1.
 CC Pfam; PF00289; CPase_L_chain; 1.
 CC TIGRFAMs; TIGR00514; accC; 1.
 CC PROSITE; PS00866; CPASE_L; 1.
 CC PROSITE; PS00867; CPASE_2; 1.
 CC Fatty acid biosynthesis; Ligase; Biotin; ATP-binding; 3D-structure;
 CC Complete proteome.
 CC NP_BIND 163 168 ATP (POTENTIAL).
 CC ACT_SITE 292 292 POTENTIAL.
 CC CONFLICT 260 261 CA -> SR (IN REF. 2).
 CC CONFLICT 313 313 L -> M (IN REF. 1).
 CC STRAND 4 7
 CC HELIX 11 24
 CC TURN 25 25
 CC STRAND 27 33

Db 3 EKVLIAARGIAIRILRACKELGIKTVAVHSTADREIMHLSLADESVCIG-PAPATQSYL 61
 QY 73 DIDEITCAAKKADAIYPGYFLSENAQALARECAENGLTIFGTPTEVLDLTGDKSRVAT 132
 Db 62 QIPAITAAAEVTCATATFGYGLFNAADFAEGIERSGFTFVGTAEVIRKMGDKVSAKD 121
 QY 133 AAKKAGLPVLAESTPSKNIDE--IVKSAEGQTYPIPVKAVAGGGGRMRVFASPFDELKRL 190
 Db 122 AMKRAGVPTVPVGGDGLPDEDEETALAEVGPVPIKAAGGGGGGRMRVYVDESELIKS 181
 QY 191 ATEASREAAFGDGAAYVERAVINPQHLEVOILQDHTGEVHLYERDCSLQRRHKVYE 250
 Db 182 AKLTRTEAGAAFPNPMVILEKFTNPRHVEQVLSQGGNAIHLGDRDCSLQRRHKVIE 241
 QY 251 IAPAOHLDELDRICADAFKFCRSIGYOGAGTVEFLVDEKGNHVFEMNPRIOQVHTVT 310
 Db 242 EAPAPGIDEKARQEVFARCVQACIEIGYRCAGTFEFL-ENGFRFYIENWTRVQVPEPVS 300
 QY 311 EEVTEVDLYKQMRILAAATGATLKLGLTQDKIKTHGAALOCRTITPDNNGFRDPTGTTIA 370
 Db 301 EMTVGDVIVKEMLRISAG--EKLSTRQEDVWIRGHALECRINAEDPKT-FMPSPGVKVH 356
 QY 371 YRSPGGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFETAVARAQRALAEFTVSGVAT 430
 Db 357 FHPAGGNGVRVSHLYSGYSVPPNDSLVGKVITYGADRDEALARMNALDELIVDGIKT 416
 QY 431 NTGFLRALREEDF 444
 Db 417 NTELHKDLVRDAAF 430

RESULT 15

MCCA_HUMAN
 ID MCCA_HUMAN STANDARD; PRT; 725 AA.
 AC Q96RQ3; Q9H959; Q9NS97;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor
 DE (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha
 DE subunit) (3-methylcrotonyl-CoA:carbon dioxido ligase alpha subunit).
 GN MCCC1 OR MCCA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid:9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANTS MCGI ARG-325 AND SER-385.
 RX PubMed=11170888;
 RA Gallardo M.E., Desvial L.R., Rodriguez J.M., Esparza-Gordillo J.,
 RA Perez-Cerda C., Perez B., Rodriguez-Pombo P., Criado O., Sanz R.,
 RA Morlon D.H., Gibson K.M., Le T.P., Ribes A., Rodriguez de Cordoba S.,
 RA Ugarte M., Penalva M.A.;
 RT "The molecular basis of 3-methylcrotonylglycinuria, a disorder of
 RT leucine catabolism.";
 RL Am. J. Hum. Genet. 68:334-346(2001).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT HIS-464.
 RX MEDLINE=21295033; PubMed=11401427;
 RA Obata K., Fukuda T., Morishita R., Abe S., Asakawa S., Yamaguchi S.,
 RA Yoshino M., Ihara K., Murayama K., Shigemoto K., Shimizu N., Kondo I.;
 RT "Human biotin-containing subunit of 3-methylcrotonyl-CoA carboxylase
 RT gene (MCCA): cDNA sequence, genomic organization, localization to
 RT chromosomal band 3q27, and expression.";
 RL Genomics 72:145-152(2001).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT MCGI PHE-535.
 RX MEDLINE=21299419; PubMed=11406611;
 RA Holzinger A., Roeschinger W., Lagler F., Mayerhofer P.U., Lichtner P.,
 RA Rattenfeld T., Thuy L.P., Nyhan W.L., Koch H.G., Muntau A.C.,
 RA Roscher A.A.;
 RT "Cloning of the human MCCA and MCCB genes and mutations therein reveal

the molecular cause of 3-methylcrotonyl-CoA: carboxylase
 deficiency.";
 Hum. Mol. Genet. 10:1299-1306(2001).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS MCGI VAL-289; SER-385; PRO-437 AND
 HIS-532.
 RX PubMed=11181649;
 RA Baumgartner M.R., Almashanu S., Suormala T., Obie C., Cole R.N.,
 RA Packman S., Baumgartner E.R., Valle D.;
 RT "The molecular basis of human 3-methylcrotonyl-CoA carboxylase
 RT deficiency.";
 RL J. Clin. Invest. 107:495-504(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
 RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
 RA Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 TISSUE=Skeletal muscle;
 MEDLINE=22388257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- CATALYTIC ACTIVITY: ATP + 3-methylcrotonyl-CoA + HCO(3)(-)= ADP +
 CC phosphate + 3-methylglutaconyl-CoA.
 CC -!- COFACTOR: Biotin.
 CC -!- PATHWAY: Leucine catabolism.
 CC -!- SUBUNIT: Probably a dodecamer composed of six biotin-containing
 CC alpha subunits and six beta subunits.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -!- DISEASE: Defects in MCCC1 are the cause of 3-
 CC methylcrotonylglycinuria type I (MCGI) [MIM:210200]; also
 CC designated CGA or CG2. MCGI is a recessive disease that is
 CC characterized by muscular hypotonia and atrophy, probably of
 CC spinal origin.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF310972; AAG53095.1; -
 CC EMBL; AB029826; BAA99407.1; -
 CC EMBL; AF297332; AAK67986.1; -
 CC EMBL; AF310339; AAG50245.1; -
 CC EMBL; AK023051; BAB14377.1; -
 CC EMBL; BC004214; AAH04214.1; -
 CC EMBL; BC004187; AAH04187.1; -
 CC Genew; HGNC:6936; MCCC1.

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DR GK: Q96RQ3; -.
DR MTM; 210200; -.
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DR GO: GO:0009374; F:biotin binding activity; NAS.
DR GO: GO:0004485; F:methylcrotonyl-CoA carboxylase activity; NAS.
DR GO: GO:0006768; P:biotin metabolism; NAS.
DR GO: GO:0006552; P:leucine catabolism; NAS.
DR InterPro: IPR001882; Biotin attach.
DR InterPro: IPR005482; Biotin carb C.
DR InterPro: IPR000089; Biotin lipoyl.
DR InterPro: IPR005479; CPase_L_D2.
DR InterPro: IPR005481; CPase_L_N.
DR Pfam: PF02785; Biotin carb C; 1.
DR Pfam: PF00364; biotin lipoyl; 1.
DR Pfam: PF02789; CPase_L_D2; 1.
DR Pfam: PF02786; CPase_L_D2; 1.
DR PROSITE: PS00188; BIOTIN; 1.
DR PROSITE: PS00867; CPASE_2; 1.
DR PROSITE: PS00867; CPASE_2; 1.
DR Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide;
DR Disease mutation; Polymorphism.
FT TRANSIT 1 47 MITOCHONDRION (POTENTIAL).
FT CHAIN 48 725 METHYLCROTONYL-CoA CARBOXYLASE ALPHA
FT NP_BIND 209 214 ATP (POTENTIAL).
FT ACT_SITE 339 339 BY SIMILARITY.
FT BINDING 681 681 BIOTIN (BY SIMILARITY).
FT DOMAIN 538 541 POLY-SER.
FT DOMAIN 713 718 POLY-GLU.
FT VARIANT 289 289 A -> V (in MCGI; mild form).
FT VARIANT 325 325 /FTid=VAR_012785.
FT VARIANT 339 339 M -> R (in MCGI).
FT VARIANT 385 385 /FTid=VAR_012786.
FT VARIANT 437 437 R -> S (in MCGI; severe form).
FT VARIANT 464 464 /FTid=VAR_012787.
FT VARIANT 464 464 L -> P (in MCGI; severe form).
FT VARIANT 532 532 /FTid=VAR_012788.
FT VARIANT 535 535 P -> H.
FT VARIANT 535 535 /FTid=VAR_012789.
FT VARIANT 535 535 D -> H (in MCGI; severe form).
FT VARIANT 535 535 /FTid=VAR_012790.
FT VARIANT 535 535 S -> F (in MCGI; asymptomatic form).
FT CONFLICT 469 469 /FTid=VAR_012791.
FT SEQUENCE 725 AA; 80433 MW; B847CBB80606B6C0 CRC64;
Query Match 15.7%; Score 911; DB 1; Length 725;
Best Local Similarity 36.5%; Pred. No. 1.2e-41;
Matches 210; Conservative 96; Mismatches 204; Indels 66; Gaps 9;
QY 4 HTSSILPAFKKILVANRGEIIVAFRAALETGAATVATYPRDGRSGFHSFASAVRIGT 63
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QY 64 EGSPVKAYLDIDDIITGAARKKADAIYPGYGLFSENAQLARECAENGITFIPTPEVLDL 123
DB 101 APSQ-QSYLSMEKILTOVAKTSAQAHPCCGLFSENMEFAELCKQGGIIFIGPPPSAIRD 159
QY 124 TGDGRVATAAKAGLPVLAESTPKNIDEIVKS-AEGQTYPIFVKAVAGGGGGRMRFVA 182
DB 160 MGIKSTKSIMAAAGVPVVEGVHGEDQSDCLKEHARRIGYIPVMIKAVRGGGGKGMIVR 219
QY 183 SPDELRLKLAATESRAEAAFGAGVYVERAVINPOHIEVQILGDHTGEVVHLYERDCSLQ 242
DB 220 SQEFTQEQLESARREAKKSFNDDAMLEKFEVDTPRHEVQVFGDHGNAVYLFERDCSVQ 279
QY 243 RHQKQVETAPAOHLDPDLDRICADAVKFCRSGYOGAGTVFELVDEKGNHVFTEMNPR 302
DB 280 RHQKILIEAPAGPKTSEVKRKLGEAAVRAAKAVYVAGTVFETMDSKHNFCEFMENR 339
QY 303 IQVEHTVTEVEVDLVKAQMLAAGATLKEGLTQDKIKTHGAALQCKRITTEDPNNNGFR 362
DB 340 LQVEHPVTMETITGTDIVIEWQLRIAG---EKIPLSQEETLQGHAFARIYAEDFSNNFM 396

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QY 363 PDTGTITAYRSP-CGAGVRLDGAQALGGEITTAHFDSDMLVKMTCRGSDFFETAVARAQALA 421
DB 397 PVAGPIVHLSTPRADPSTRIETGVROGDEVSVHYDPMIAKLIVVWAADRQAALTKLYSLR 456
QY 422 EFTVSGVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRILDYLDVDT 481
DB 457 QYNIVGLPTNIDFLNLSGHPEPAGNVHTDFIQH----- 492
QY 482 VNKPHGVPRKDVAAPIDKLPNPKDLPLPRGSRDLKQLGPAAFAFARDLREQDALAVTDTTF 541
DB 493 -----KOLLLSRKAALK-ESLCCQAALGLILKEK---AMTDITF 527
QY 542 RDAH-----QSLLATRVRSFALKPAAEAVA 566
DB 528 LQAHQSPFSSSSGRRLNISYTRNMTLKDGKNVA 563

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Search completed: September 24, 2003, 15:56:06
Job time : 21.3631 secs

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OM protein - protein search, using sw model

Run on: September 24, 2003, 15:27:07 ; Search time 17.8668 Seconds
(without alignments)
2699.668 Million cell updates/sec

Title: US-09-974-973A-19

Perfect score: 5788

Sequence: 1 MSTHTSSTLPAPKKILVANR.....RVVPATKVEGDLIVVVS 1140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	5788	100.0	1140	3	US-09-220-081-2
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3	3483	60.2	1124	4	US-08-311-731A-10
4	2454	42.6	1134	4	US-09-134-001C-3428
5	2174	37.6	973	4	US-09-107-532A-4810
6	1192	20.6	694	4	US-09-433-043B-126
7	1083	18.7	456	4	US-09-634-238-276
8	1043.5	18.0	593	4	US-09-433-043B-122
9	1036.5	17.9	447	1	US-08-611-107-6
10	1036.5	17.9	447	2	US-08-422-560A-6
11	1036.5	17.9	447	3	US-08-468-793-6
12	1004.5	17.4	453	1	US-08-611-107-8
13	1004.5	17.4	453	2	US-08-422-560A-8
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15	1002.5	17.3	453	4	US-09-433-043B-121
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17	995.5	17.2	453	1	US-08-476-537-6
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21	967.5	16.7	474	4	US-09-328-352-7562
22	966.5	16.7	1116	4	US-09-252-991A-24374
23	952	16.4	605	4	US-09-433-043B-123
24	938	16.2	448	1	US-08-074-121-3
25	938	16.2	448	5	PCT-US94-06447-3
26	937	16.2	427	1	US-07-956-700B-3
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28	937	16.2	427	1	US-08-485-607-3	Sequence 3, Appli
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31	935.5	16.2	454	4	US-09-198-452A-197	Sequence 197, App
32	935.5	16.2	701	4	US-09-252-991A-27999	Sequence 27999, A
33	926	16.0	536	3	US-08-662-344-2	Sequence 2, Appli
34	924.5	16.0	465	4	US-09-252-991A-26980	Sequence 26980, A
35	924	16.0	449	1	US-08-074-121-6	Sequence 6, Appli
36	924	16.0	449	5	PCT-US94-06447-6	Sequence 6, Appli
37	901	15.6	676	4	US-09-252-991A-26143	Sequence 26143, A
38	899	15.5	670	4	US-09-328-352-6725	Sequence 6725, Ap
39	891	15.4	652	4	US-09-328-352-5587	Sequence 5587, Ap
40	889	15.4	573	4	US-09-328-352-6420	Sequence 6420, Ap
41	858.5	14.8	1212	4	US-09-252-991A-26616	Sequence 26616, A
42	851.5	14.7	461	4	US-09-433-043B-125	Sequence 3604, App
43	843.5	14.6	722	4	US-09-433-043B-125	Sequence 125, App
44	841	14.5	612	4	US-09-252-991A-19134	Sequence 19134, A
45	835.5	14.4	453	4	US-09-252-991A-19829	Sequence 19829, A

ALIGNMENTS

RESULT 1

US-09-220-081-2
; Sequence 2, Application US/09220081
; Patent No. 6171833
; GENERAL INFORMATION:
; APPLICANT: Sinskey, Anthony J.
; APPLICANT: Lessard, Philip A.
; APPLICANT: Willis, Laura B.
; APPLICANT: Stephanopoulos, Gregory
; TITLE OF INVENTION: Pyruvate Carboxylase from Corynebacterium glutamicum
; FILE REFERENCE: 1533.0790000
; CURRENT APPLICATION NUMBER: US/09/220,081
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-220-081-2

Query Match	100.0%	Score 5788;	DB 3;	Length 1140;
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Db 421 AEFTVSGVATNGFLLRALLREEDFTSKRTATGFIADHPHLLQAPPADDEQGRLLDVLADY 480
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RESULT 2

US-09-677-575-2
; Sequence 2, Application US/09677575
; Patent No. 6403351
; GENERAL INFORMATION:
; APPLICANT: Sinskey, Anthony J.
; APPLICANT: Lessard, Philip A.
; APPLICANT: Willis, Laura B.
; APPLICANT: Stephanopoulos, Gregory
; TITLE OF INVENTION: Pyruvate Carboxylase from *Corynebacterium glutamicum*
; FILE REFERENCE: 1533.0790000
; CURRENT APPLICATION NUMBER: US/09/677,575
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 09/220,081
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1140
; TYPE: prt
; ORGANISM: *Corynebacterium glutamicum*

US-09-677-575-2

Query Match 100.0%; Score 5788; DB 4; Length 1140;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 LDLTGDKSAVTAATAAKAGLPVLAESTPSKNIDEIVKSAEGQTYPIFVKAVAGGGGGMRF 180
QY 181 VASPDRLRLKLAETASREAAAFDGAIVYVERAVINPQHTIEVQILGSDHTGEVHLYERDCS 240
Db 181 VASPDRLRLKLAETASREAAAFDGAIVYVERAVINPQHTIEVQILGSDHTGEVHLYERDCS 240
QY 241 LORRHQKVVEIAPAHQLDPELDRCADAVKFCRSIGYOGAGTVFELVDEKGNHVFIEMN 300
Db 241 LORRHQKVVEIAPAHQLDPELDRCADAVKFCRSIGYOGAGTVFELVDEKGNHVFIEMN 300
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Db 301 PRIQVEHTVTEEVTEVDLVKAQMLAAGATLKGELGTODKIKTHGAALQCRITTEDPNNG 360
QY 361 FRPDGTTITAYRSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFTETAVARAQAL 420
Db 361 FRPDGTTITAYRSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFTETAVARAQAL 420
QY 421 AEFTVSGVATNGFLLRALLREEDFTSKRTATGFIADHPHLLQAPPADDEQGRLLDVLADY 480
Db 421 AEFTVSGVATNGFLLRALLREEDFTSKRTATGFIADHPHLLQAPPADDEQGRLLDVLADY 480
QY 481 TVNKHGVRPKDVAAPIDKLPNIKLPPLRGSRDLKQLGPAAFARDLREQDALAVTDIT 540
Db 481 TVNKHGVRPKDVAAPIDKLPNIKLPPLRGSRDLKQLGPAAFARDLREQDALAVTDIT 540
QY 541 FRAHOSLLATVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPDWRDLE 600
Db 541 FRAHOSLLATVRSFALKPAAEAVAKLTPELLSVEAWGGATYDVAMRFLFEDPDWRDLE 600
QY 601 LREAMPNVNIOMLLRGNTVGYTPYDPSVCRAVFEAAASSGVVDIFRIFDALNDVSOMRPA 660
Db 601 LREAMPNVNIOMLLRGNTVGYTPYDPSVCRAVFEAAASSGVVDIFRIFDALNDVSOMRPA 660
QY 661 IDAVLETNTVAEAVAMAYSGDLSDPNEKLYTLDYLLKMAEEIVKSGAHLAIKDMAGLLR 720
Db 661 IDAVLETNTVAEAVAMAYSGDLSDPNEKLYTLDYLLKMAEEIVKSGAHLAIKDMAGLLR 720
QY 721 PAAVTKLVTLALRREFDLPVHVHTHDTAGGOLATYFAAAQAGADAVDGSAPLSGTTSQPS 780
Db 721 PAAVTKLVTLALRREFDLPVHVHTHDTAGGOLATYFAAAQAGADAVDGSAPLSGTTSQPS 780
QY 781 LSAIVAAFAHTRDRTGSLSEAVSDLEPYWEAVRGVLYLPESGTPGPTGRVYRHEIPGGOL 840
Db 781 LSAIVAAFAHTRDRTGSLSEAVSDLEPYWEAVRGVLYLPESGTPGPTGRVYRHEIPGGOL 840
QY 841 SNLRAQATLGLADRFELIEDNYAAVNEMLRPTKVTTPSSKVVGDALHLVAGVDPADF 900
Db 841 SNLRAQATLGLADRFELIEDNYAAVNEMLRPTKVTTPSSKVVGDALHLVAGVDPADF 900
QY 901 AADPKYDIPDSVIAFLRGELGNPPGGWPELRTALRGSRSEKAPLTVPEEQOAHLDA 960
Db 901 AADPKYDIPDSVIAFLRGELGNPPGGWPELRTALRGSRSEKAPLTVPEEQOAHLDA 960
QY 961 DSKERRNSLNRLFPKPTPEEFLEHRRRFGNTSALDDREFFYGLVEGRETLLRLPDVRTP 1020
Db 961 DSKERRNSLNRLFPKPTPEEFLEHRRRFGNTSALDDREFFYGLVEGRETLLRLPDVRTP 1020

QY 1021 LLVRLDAISEPDDKGMNVANVNGQIRPMRVDRSVESVTATAEAKDSSNKGHVAAPFA 1080
 Db 1021 LLVRLDAISEPDDKGMNVANVNGQIRPMRVDRSVESVTATAEAKDSSNKGHVAAPFA 1080
 QY 1081 GVVTVTVAGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAAATKVEGGDLIVVVS 1140
 Db 1081 GVVTVTVAGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAAATKVEGGDLIVVVS 1140

RESULT 3

US-08-311-731A-10
 ; Sequence 10, Application US/08311731A
 ; Patent No. 6583266
 ; GENERAL INFORMATION:
 ; APPLICANT: SMITH, DOUGLAS
 ; APPLICANT: MAO, JEN-I
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
 ; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
 ; NUMBER OF SEQUENCES: 411
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
 ; STREET: 600 ATLANTIC AVENUE
 ; CITY: BOSTON
 ; STATE: MASSACHUSETTS
 ; COUNTRY: USA
 ; ZIP: 02210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/311,731A
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GATES, EDWARD R.
 ; REGISTRATION NUMBER: 31,616
 ; REFERENCE/DOCKET NUMBER: C0044/7125
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/720-3500
 ; TELEFAX: 617/720-2441
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1124 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHEetical: YES
 ; ORIGINAL SOURCE:
 ; ORGANISM: MYCOBACTERIUM TUBERCULOSIS
 ; US-08-311-731A-10

Query Match 60.2%; Score 3483; DB 4; Length 1124;
 Best Local Similarity 62.2%; Pred. No. 7.7e-267;
 Matches 698; Conservative 151; Mismatches 251; Indels 22; Gaps 9;
 QY 12 FKKILVANGEIAVRAALETGAATVAIYPREDRSGSRSPASEAVRLGTGSPVKAY 71
 Db 2 FSKVLVANGETAIRAFRAAYELGVGTVAIYPYEDRNSOHLKADESYQIGDIGHPVHAY 61
 QY 72 LDIDEITGAAKYKADAIYPGYGLFSENQALARECAENGITFTIGPTPEVLDTGDKSRAY 131
 Db 62 LSVDEIVATARRAGADAIYPGYGLFSENPDLAACAAGISFVGPSAEVLEAGNSRAI 121
 QY 132 TAAKAGLPLVAESTSKNIDEIVKSAEGQTYPIFKVAVAGGGGGRMRFVSPDELKKA 191
 Db 122 AAAREAGLPLVMSAPSASDELSSAAGMPFLEFKAVAGGGGGRMRFVSPDELKKA 191
 QY 192 TEASRAEAAFGDGVYVERAVINPOHIEVQILGDHTGEVHLHYERDCSLQRHOKVWE 251
 Db 192 TEASRAEAAFGDGVYVERAVINPOHIEVQILGDHTGEVHLHYERDCSLQRHOKVWE 251

Db 182 EAASREASAPGDPVTYVLEQAVINPRHLEVOILADNLDVLIHLVERDCSVORRQKVTEL 241
 QY 252 APAQHLDELDRICADAVKFCRSIGYAGTVEFLVDEKGNHVFIEPNRIQVHEHTVTE 311
 Db 242 APAHLDAELRYKMCVDAVAFARHIGYSCAGTVEFLDERGEYVFIEPNRQVHEHTVTE 301
 QY 312 EVTEVDLVKACMRILAAGATIKELGTQDKIKTHGAALQCRITTEDPNNNGFPDPDTGITWAY 371
 Db 302 EITDVIDLISQILRIARAGETLEQLGRQEDIAHPGAALQCRITTEDPANGERP-TRAGSAR 360
 QY 372 RSPGGAGVRLDGAAGLGEITAHFDSMLVKM-----TCRGSDFETAVARAQALAEPTVS 426
 Db 361 CDPAPVPVSATAAP-----TWNRNQPVRLRHAGQADLSGRDLPATVSRARRALAEFIR 415
 QY 427 GVATNIGFLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEOGRILDYADYVTKNPH 486
 Db 416 GVSTNIPFLQAVLDDPDRAGRVTSFIDERPQLLTARASADRGTKIKFLNADYVNNPY 475
 QY 487 GVRPKOVAAPDKLPNIKDLPL-----PRGSRDLKQIGPAFAFADLREQDALAYDTTTER 542
 Db 476 GSREFTI-YFDDKLP---DLDLRAAPPAGSKQRLVKGPGFARWLRESAAVGVDTTTER 531
 QY 543 DAHQSLLATRVRSFALPAAEAVALKTPPELLSVKAWGATYDVAMRFLFEDPMDRLDEL 602
 Db 532 DAHQSLLATRVRTSGLSRVAPYLARTMPQLLSVECWGATYDVVALRFLKEDPWERLATLR 591
 QY 603 EAMPNVNIOMLLRGRTVGYTPPDSVCRAPFVKAASGVVDIFRIFDALNDVSMRPAID 662
 Db 592 AAMPNICLOMLLGRNTVGYTPPEIYTSFAVQVQATATGIDIERIFDALNNIESMRPAID 651
 QY 663 AVLENTNTAVAEVAMAYSGDLSDPNEKLYTLIDYLLKMAEEIVKSGAHLAKDMAGLLRPA 722
 Db 652 AVRETSIAIEVAMCYTGDLTDQGEQYTLIDYLLKLAQIVDAGAHVLAINDMAGLLRPP 711
 QY 723 AVTKLVLTALRREFDLPVHVTHTAGGQATYFAAAQAGADAVDAGASAPLSGTSQPSLS 782
 Db 712 AAQRLVSALRSRFDLPVHLHTHTDTPGGQLASYVAWAHAGADAVDGAAPLAGTTSQPSLS 771
 QY 783 AIVAAPFAHTRDTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGTPGVYHEHPGGQSLN 842
 Db 772 SIVAAAHAETDYLGLSLSAVCALEPYWEALKRVYAPFESGLPGTPGVYHEHPGGQSLN 831
 QY 843 LRAQATAGLGLARFELIEDNYAAVNEMLGRPTKVPSSKVVGDLALHLVAGVDPADFAA 902
 Db 832 LRQQAIALGLGRFEELEAYAGADRVGLRVLVKVPYTKVVGDLALVAGVSADEFAS 891
 QY 903 DPQYDIPDSVIAFLRGEELNPPGGWPEPLRTRALEGRSEKAPLTPVPEEQAHLDADD 962
 Db 892 DPARFGIPESVLGLRGLGELDPPGGWPEPLRTAALAGRGAAR-PTAQLAADDEITALSSVG 950
 QY 963 SKERRNSLRLPLPKPTEEFLEHRRRGNTSALDDREFFYGLVEGRETLRLPDVPTPL 1022
 Db 951 AK-RQATLNRLLFPSPKTEENEHREAYGDTQSLSANQFFYGLRQGEHRRVKL-ERGVELL 1008
 QY 1023 VRLDAISEPDDKGMNVANVNGQIRPMRVDRSVESVTATAEAKDSSNKGHVAAPFAV 1082
 Db 1009 IGLDAISEPDDKGMNVANVNGQIRPMRVDRSVESVTATAEAKDSSNKGHVAAPFAV 1068
 QY 1083 VTVTVAGDEVKAGDAVAIIEMKMEATITASVDGKIDRVV 1124
 Db 1069 VTVGVCGVRVAGAGTATIAEMKMEAPITAPVAGTVERVAV 1110

RESULT 4

US-09-134-001C-3428
 ; Sequence 3428, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C

Db	841	GOYSNLQAKSLGLGERFDEVKEMRYRVNLFGLGVKVPSSKVVGMALYVQDLD	900
QY	897	PADFRADPOKYDIPDSVAFUFLRGLGNPPGWPPELFRTRALEGRSEKAPLTVPEBEQA	956
Db	901	EDTVINDGYKLDFFPESVVSFFKGDIGQPVNGFNKQLQDVILKQOQ---	956
QY	957	HLADAD-----DSKERNSLNRLLPKPTFEFLHRRRGNTSALDDREFFYGLV	1005
Db	957	PVDFFAIRQLSDIOQDEVTQDIISYVLYPKVKQYIOTKEQFGNVSLDTPFLFGMR	1016
QY	1006	EGRETLIRLPDVRTPLLVRLDAISPDGDKMRNVNVANVGQIRPMVRDRSVESVTATAE	1065
Db	1017	NGETVEIEI-DTGKRLIKLEITSEPDENGKRTIYAMNGOARIYIQDENVKINAVKP	1075
QY	1066	KADSNKGHVRAFPAGVVT-VTVAGDEVKAGDAVAIEAMKMEATTITVSDGKIDRVV	1124
Db	1076	KADKSNPHIGAQMGSVTVKVSQVDEQANQPLLIETAMKMETTIQAPFDGLIKQINV	1135
QY	1125	PAATKVEGGDLIVV	1139
Db	1136	ANGDAIATGDLVEI	1150

RESULT 5

US-09-107-532A-4810

; Sequence 4810, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESS: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 4810:

SEQUENCE CHARACTERISTICS:

LENGTH: 973 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...973

SEQUENCE DESCRIPTION: SEQ ID NO: 4810:

QY	9	LPAPFKILVANGETIAVRAFAALGTGAATVAIYPRDRGSHFSFSEAVRIGTEGSPV	68
Db	6	LQIKKILVANGETIAIFRAAELNISTVAIYSDNEDKSLHRYKADESILVGSDLGPA	65
QY	69	KAYLIDELIGAAKKVADAIYGYGFLSENAQLARECAENGTIFIGTPEVLDTLTKDS	128
Db	66	ESYLNTERIEIIVLRAGVDAIHPGYGFLSENEQFARRCAEBSIKFIPGLEHLDMDGKV	125
QY	129	RAVTAAKAGLPVL-AETSPKNDIDEIVKSEGGOTYPIFKAVAGGGGGRMRVFASDEL	187
Db	126	KARTTAIANLPVPIGTDPETSEFAAQFANEAGYPLMIKATSGGGGKGMIRVRESSEL	185
QY	188	RKLAIEASKEAEAFDGCADVVERAVINPOHIEVQILGHDGTGEVVLHYERDCSLORHQK	247
Db	186	EDAFHRAKSEAKSGNSEVIERIYNPKHIEVQVIGDEFGNIIHLYERDCSVORHQK	245
QY	248	VVEIAPAOHLDELDRICADAVKFCRSIGYGAGTVEFLV--DEKGNHVFIEIENPRIOV	305
Db	246	VVEVAPSVGLSNKLRICDAAIQIMENIKYVNAGTVEELVSGDE---FFIEVNPVQV	302
QY	306	EHTVTEEVTEVDLYKAQMLAAGATL--RELGTQDKIKYTHGAALQCRITTEDPNNGFR	362
Db	303	EHTIETMGIDIVKTLVANGSELGDKTSMPPQONEIQLTGVAIQCRITTEDPTNDPM	362
QY	363	PDGTGITAYRSPGGAGVRLD-GAALQGEITAIHSDMLVKMTCRGSDFFETAVARAQALA	421
Db	363	PDGFTIIAYRSGGFGVRLDAGDFQAEKISPYDLSLVKLSHVSFKQAEKEMKERSLR	422
QY	422	ETVSGVATNIGTLRALLREEDFTSKRIATGFIADHPHLLQAPPADDEQGRIDLYADVT	481
Db	423	EMRIGVKTNIPFLINVRNDKRSRGDYTKFIETPELFDIAPTLDRGKTKLEYIGNVT	482
QY	482	VNKHGV--RPKDVAAPDKLPNKIDPLPR--GSRDLKQLGPAFAFARDLRQDALAVT	537
Db	483	INGFNVEKRPKP-EYESTKIPKISQKKINQLGFTKQILEQHGPTGVTNVRVQEDVLIT	541
QY	538	DTTFDAHQSLIATVRSFALKPAEAAVAKITPELLSVEAWGATYDVAMRFFEDPWR	597
Db	542	DTTFDAHQSLIATVVRTKOMNTASKTAEVFKDSFSLEMGWATFDVAYNFLKENPWR	601
QY	598	LDELREAMPNNIOMLGRNTVGYTYPDSVCRAFVKAASSGVDFIRFDALNDVSQM	657
Db	602	LERLRKATPNVLFQMLLRASNAVGYKNYPDNVKKFVHESAKAGVDVFRFDSLNVDQM	661
QY	658	RPAIDAVLETTVAEAVAMAYSGD-LSDPNKELYTLIDYLKMAEIEIVKGAHILAKOMA	716
Db	662	KVAEAVQEAG-WYSEGTICYTGDILNAERSNTYTLIDYVVKMAKELEREGFHILAKDMA	720
QY	717	GILLPAAVTKLVLTALRREFDLPVHVHPHTDAGGOLATYFAAQAAGADAVDGASAPLSGTT	776
Db	721	GILLPKAAYELIGELREATHPLHLTHDTSGNLLIYKQAIIDAGVDIIDTAVASMSGLT	780
QY	777	SQPSLSIAVAFAHTRDRTGLSLEAVSDLEPYVEAVRGLYLPFESGTPGPTGRVYRHEIP	836
Db	781	SQPSANSLSYALNGFPNRLRTDIDGLELSHYVSVRPYYADFESDIKSPNTEIYQHEMP	840
QY	837	GGQISNLRQAATGLADREFLEIDNTVAANVEMGRPTKVTTPSSKVVGDLALHLVAGVD	896

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3428

LENGTH: 1154

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3428

Query Match 42.6%; Score 2464; DB 4; Length 1154;

Best Local Similarity 45.4%; Pred. No. 4e-186;

Matches 524; Conservative 197; Mismatches 400; Indels 34; Gaps 14;

131	Db	AGDLFADLHLPOCDALRENGAAIOCRITTEDPENNFMPDGTINTYSPGFGIRLDVG	190
384	QY	AAQLGGEITAHFOSMLYKMICRGSDPETAVARAQRALAEFTVSGVATNIGRLALLREED	443
191	Db	NAYAGAVVSPYFOSLLWKASVHAFSPFAAVAKMRALHEFOITGVKTNVALEHLLATQT	250
444	QY	FTSKRIATGADHPHLLQAPPADDEQGRILDYLDATVNNKPHGV-REKDYAAPIDKLPN	502
251	Db	FRTGEAETATDAHPPELLQVQAKPDIASRLWYISDVTVNGFKGVERQSQKYP--ELQY	308
503	QY	IKDLPLPRGSRD--RLKOLGPAAFAFDLREQDALAVTDTTFRDAHQSLIATRYSPALK	559
309	Db	TRFPAAKPQTDLVALLKNGEQAQVTDVWKAKHPALLTDTTFRDAHQSLFATRMTRDML	368
560	QY	PAEAEVAKLTPELLSVEMAGGATYDVAMREFLEFDPDWRDLDELREAMPNVNTOMLLRGNT	619
369	Db	TVAEIDMGNGLPLNLFMSVEMWGATFDVAYRELINEDFPWRLKKLRAALPHTLLQMLFRGSNA	428
620	QY	VGTYTPDPSYCFRAFVKEAASGVDFRI	647
429	Db	VGYONYPDNVTKAFINQOANDGVDFRI	456

RE: 09-433-043B-122
 US-09-433-043B-122
 ; Sequence 122, Application US/09433043B
 ; Patent No. 6399342
 ; GENERAL INFORMATION:
 ; APPLICANT: HASELKORN, ROBERT
 ; APPLICANT: GORNICKI, PIOTR
 ; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-COA CARBOXYLASE

ETTL; TITLE

```

/ FILE REFERENCE: ARCD:3380US
/ CURRENT APPLICATION NUMBER: US/09/433,043B
/ CURRENT FILING DATE: 1999-10-25
/ PRIOR APPLICATION NUMBER: 08/475,879
/ PRIOR FILING DATE: 1995-06-07
/ PRIOR APPLICATION NUMBER: 07/956,700
/ PRIOR FILING DATE: 1992-10-02
/ NUMBER OF SEQ ID NOS: 128
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 122
/ LENGTH: 593
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Peptide
US-09-433-043B-122

Query Match      18.0%; Score 1043.5; DB 4; Length 593;
Best Local Similarity 44.8%; Pred. No. 4.4e-74;
Matches 229; Conservative 81; Mismatches 180; Indels 23; Gaps 5;

QY      12   FKILVANRGEIAVRAFRALAEATVAIVLPREDRGSFHRSFASAEVRIGTEGSPVKAY 71
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      3   FDKILIANRGEIALRILCAEENGIIATIAVHSITVDNALHVQLADEAVCIIG-EFASAKSY 61

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Db      :
        :
62      LNIPNIIAAALTRNASAIHPGYGFLSENAKFAEICADHIIAFIGTPEAIRLMDGDKSTAK 121
        :
122     TAAATACI DVA A DGRCKNTD ETLVCA DQGVCTYUWNAAGCCGGCGGT DVA 100
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[illegible]

QY 311 EEVTEVDLVKAQMLAAGATLKEGLTQDKIKTHGAALOCRTTDPNNGFRPDTGTITA 370
 Db 302 EMVTGVDLLVEQIRIAQGERLR--LTQDQVVLGRHAIECRINAEDPDHFRPAPGRISG 358
 QY 371 YRSPGGAGVRLDGAAGLGGSEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTVSGVAT 430
 Db 359 YLPPGGPGVRIDSHVTDYQIPPYDSLSLGLKLVWGPDRATAINRMKRALRECAITGLPT 418
 QY 431 NIGFLRALLREEDFTSKRIATGFIADPHLLQAPPADDEQGRILDYLA-----478
 Db 419 TIGFHQRIMENPQLQGNVSTSVQVE---MNPDLDFNEIRQLLTITIAQTDIAEVLTKSD 474
 QY 479 --DVTNKPGRVPRKDVAAIDKLPNIKOLPLP 509
 Db 475 DFLTVRKAVGVNNSVVPVVTAPLSGVGSLP 507

RESULT 9

US-08-611-107-6
 ; Sequence 6, Application US/08611107
 ; Patent No. 5801233
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselkorn, Robert
 ; APPLICANT: Gornicki, Piotr
 ; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
 ; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE AND USES
 ; TITLE OF INVENTION: THEREFOR
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: United States of America
 ; ZIP: 77210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: US/08/611,107
 APPLICATION NUMBER: 31
 FILING DATE: Concurrently Herewith
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US SN 07/956,700
 FILING DATE: 02-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US PCT/US93/09340
 FILING DATE: 30-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US SN 08/422,560
 FILING DATE: 14-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: ARCD:221
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 447 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

Query Match

Best Local Similarity 17.9%; Score 1036.5; DB 1; Length 447;

Matches 216; Conservative 73; Mismatches 152; Indels 5; Gaps 3;

QY 12 FKKILVANRGEIAVRAFRAALETGAATVAILYPRDRGSFHRSPASEAVRIETGSPVKAY 71
 Db 3 FDKILIANRGEIAVRIIRACEEMGIATIAVHSTVDNALHVQLADEAVCIIG-EPASAKSY 61
 QY 72 LDDEILIGAAKKVKADAIYPGYGFLSNAQLARECAENGITTFIGTPEVLDLDTGDKSRV 131
 Db 62 LNIPNIIAAALTRNASAIHPGYGFLSNAKFAETCADHIAFIPTPEAIFLMGDKSTAK 121
 QY 132 TAAKKAGLPVLAESTPSKNID-EIVKSAEGQTTPIFVKAVAGGCGRMRFVSPDELRLK 190
 Db 122 ETMOKAGVPTPGSEGLVETEQEGLELAKDIGPVMIKATAGGGGMRILVRSDFEVLK 181
 QY 191 ATASREAEAFDGAIVYVERAVINPOHIEVILGDHTGEVWHLYEDCSIORHOKVVE 250
 Db 182 FLAAGGAGAAFGNAGVIEKFTIERPHIEFQILLADNYGNVHLGERDCSIQRNQLLE 241
 QY 251 IAPAQHLDPELRDRICADAYKFCRSIGYGAGTVEFLVDEKGNHVFTEMNPRIQVEHVT 310
 Db 242 EAPSPALDSLREKMGQAAVKAQFINYTGAGTIEFLDRSGQFYFPMEMTRIQVEHPVT 301
 QY 311 EEVTEVDLVKAQMLAAGATLKEGLTQDKIKTHGAALOCRTTDPNNGFRPDTGTITA 370
 Db 302 EMVTGVDLLVEQIRIAQGERLR--LTQDQVVLGRHAIECRINAEDPDHFRPAPGRISG 358
 QY 371 YRSPGGAGVRLDGAAGLGGSEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTVSGVAT 430
 Db 359 YLPPGGPGVRIDSHVTDYQIPPYDSLSLGLKLVWGPDRATAINRMKRALRECAITGLPT 418
 QY 431 NIGFLRALLREEDFTSKRIATGFIAD 456
 Db 419 TIGFHQRIMENPQLQGNVSTSVQVE 444

RESULT 10
 US-08-422-560A-6
 ; Sequence 6, Application US/08422560A
 ; Patent No. 5910626
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselkorn, Robert
 ; APPLICANT: Gornicki, Piotr
 ; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS FOR USE
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77210-4433
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/422,560A
 ; FILING DATE: 14-APR-1995
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/956,700
 ; FILING DATE: 02-OCT-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wilson, Mark B.
 ; REGISTRATION NUMBER: 37,259
 ; REFERENCE/DOCKET NUMBER: ARCD:152/WIM
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 512-418-3000
 ; TELEFAX: 512-474-7577
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 447 amino acids
 ; TYPE: amino acid

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; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-422-560A-6

Query Match          17.9%; Score 1036.5; DB 2; Length 447;
Best Local Similarity 48.4%; Pred. No. 1e-73;
Matches 216; Conservative 73; Mismatches 152; Indels 5; Gaps 3;

QY 12 FKKILVANRGEIAVRAFRALLETGAATVAIYPREDRGSFHRSPASEAVRIGTSGSPVKAY 71
Db 3 FDKILIANRGEIALRILRACEEMGIATIAVHSTVDRNALHVQLADEAVCIIG-EPASAKSY 61

QY 72 LDIDEIIGAIAKVKADAIYPGYGLSENAQLARECAENGITFTGPTPEVLDLTDGKSRV 131
Db 62 LNPNIIAAALTNRSAIHGPGYGLSENAKFAICADHIIAFITGPTPEAIRLMDKSTAK 121

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Db 419 TIGFHORIMENPQLOGNVSTSFVQE 444

RESULT 11
US-08-468-793-6
; Sequence 6, Application US/08468793
; Patent No. 617267
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; Zip: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,793
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/422,560
; FILING DATE: 14-APR-1995
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; CLASSIFICATION: 800

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; APPLICATION NUMBER: PCT/US93/09340
; FILING DATE: 30-SEP-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:152/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-793-6

Query Match          17.9%; Score 1036.5; DB 3; Length 447;
Best Local Similarity 48.4%; Pred. No. 1e-73;
Matches 216; Conservative 73; Mismatches 152; Indels 5; Gaps 3;

QY 12 FKKILVANRGEIAVRAFRALLETGAATVAIYPREDRGSFHRSPASEAVRIGTSGSPVKAY 71
Db 3 FDKILIANRGEIALRILRACEEMGIATIAVHSTVDRNALHVQLADEAVCIIG-EPASAKSY 61

QY 72 LDIDEIIGAIAKVKADAIYPGYGLSENAQLARECAENGITFTGPTPEVLDLTDGKSRV 131
Db 62 LNPNIIAAALTNRSAIHGPGYGLSENAKFAICADHIIAFITGPTPEAIRLMDKSTAK 121

QY 132 TAAKAGLPVIAESTPSKNID-EIVKSAEGOTYPIFVKAVAGGGGRMRFVSPDELRLK 190
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Db 359 YLPPGGPGVRIDSHVYTDYQIPYDLSLIGKLIWGPDRATATNRMKRALRECAITGLPT 418

QY 431 NIGFLRALLREEDFTSKRIATGFIAD 456
Db 419 TIGFHORIMENPQLOGNVSTSFVQE 444

RESULT 12
US-08-611-107-8
; Sequence 8, Application US/08611107
; Patent No. 5801233
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas

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COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: Concurrently Herewith
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US SN 07/956,700
 FILING DATE: 02-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US PCT/US93/09340
 FILING DATE: 30-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US SN 08/422,560
 FILING DATE: 14-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: ARCD:221
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-611-107-8

Query Match 17.4%; Score 1004.5; DB 1; Length 453;
 Best Local Similarity 47.1%; Pred. No. 3.5e-71;
 Matches 209; Conservative 72; Mismatches 158; Indels 5; Gaps 3;
 QY 12 FKKILVANRGEIAVRAAPRAALETGAATVAIYPREDRGSFHRSEASEAVRIGTEGSPVKAY 71
 Db 3 FKKILVANRGEIAVRAAPRAALETGAATVAIYPREDRGSFHRSEASEAVRIGTEGSPVKAY 71
 QY 72 LDIDEIIGAIAKVKADAIYPGYGFLSENALARECAENGITFTGPTPEVLDLTGDKSRAY 131
 Db 62 LNIPNIIAALTRNSAHPGYGFLSENALARECAENGITFTGPTPEVLDLTGDKSRAY 131
 QY 132 TAAKAGPLVLAESTP-SKNIDEIVKSAEGQTYPIFVKAVAGGGRGMRFVSPDELRLK 190
 Db 122 ETMQRVGVTPIPGSDGLITDVSAAKVAEIGYPMVMIKATAGGGGRGMRLVREPADLEKL 181
 QY 191 ATASREAEAFGDDGAVYVERAVINPQHIEVQILGDHTGEVHLYERDCSLORRHOKVVE 250
 Db 182 FLAAQGEAEAFGNPGLYLEKFIDRPRHVEFQLADAYGNVHVGEDCSIQRRHOKLLE 241
 QY 251 IAPAQHLDLDRICADAVKFCRSIGYAGAGVEFLVDEKGNHVTIEMNPRIQVHEVTVT 310
 Db 242 EAPSPALSDLRKMGDAVKVAQAIGYAGAGVEFLVATGNFYEMNTRIQVHEVTVT 301
 QY 311 EEVTEVDLVKQMRALAAAGATLKEGLTQDKIKTHGAALQCRITTEPNNRFRDPTGTITA 370
 Db 359 YLPPGGPGVRVDVSHVYDIEIPYDLSLGLKLIWGWATREEARMQRALRECAITGLPT 418
 QY 431 NIGFLRALREEDFTSKRTATGFI 454
 Db 419 TUSFHQLMQMPEFLRGELYTNFV 442

RESULT 13

US-08-422-560A-8
 Sequence 8, Application US/08422560A
 Patent No. 5910626
 GENERAL INFORMATION:
 APPLICANT: Haselkorn, Robert
 APPLICANT: Gornicki, Piotr
 TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
 METHODS FOR USE
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: USA
 ZIP: 77210-4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/422,560A
 FILING DATE: 14-APR-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/956,700
 FILING DATE: 02-OCT-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Wilson, Mark B.
 REGISTRATION NUMBER: 37,259
 REFERENCE/DOCKET NUMBER: ARCD:152/WIM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512-418-3000
 TELEFAX: 512-474-7577
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-422-560A-8

Query Match 17.4%; Score 1004.5; DB 2; Length 453;
 Best Local Similarity 47.1%; Pred. No. 3.5e-71;
 Matches 209; Conservative 72; Mismatches 158; Indels 5; Gaps 3;
 QY 12 FKKILVANRGEIAVRAAPRAALETGAATVAIYPREDRGSFHRSEASEAVRIGTEGSPVKAY 71
 Db 3 FKKILVANRGEIAVRAAPRAALETGAATVAIYPREDRGSFHRSEASEAVRIGTEGSPVKAY 71
 QY 72 LDIDEIIGAIAKVKADAIYPGYGFLSENALARECAENGITFTGPTPEVLDLTGDKSRAY 131
 Db 62 LNIPNIIAALTRNSAHPGYGFLSENALARECAENGITFTGPTPEVLDLTGDKSRAY 131
 QY 132 TAAKAGPLVLAESTP-SKNIDEIVKSAEGQTYPIFVKAVAGGGRGMRFVSPDELRLK 190
 Db 122 ETMQRVGVTPIPGSDGLITDVSAAKVAEIGYPMVMIKATAGGGGRGMRLVREPADLEKL 181
 QY 191 ATASREAEAFGDDGAVYVERAVINPQHIEVQILGDHTGEVHLYERDCSLORRHOKVVE 250
 Db 182 FLAAQGEAEAFGNPGLYLEKFIDRPRHVEFQLADAYGNVHVGEDCSIQRRHOKLLE 241
 QY 251 IAPAQHLDLDRICADAVKFCRSIGYAGAGVEFLVDEKGNHVTIEMNPRIQVHEVTVT 310
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QY 431 NIGFLRALLREDEFTSKRIATGFI 454

Db 419 TLSFHQLMLQMPFLRGELYTNFV 442

RESULT 14

US-08-468-793-8
; Sequence 8, Application US/08468793
; Patent No. 6177267
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,793
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/422,560
; FILING DATE: 14-APR-1995
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; CLASSIFICATION: 800
; APPLICATION NUMBER: PCT/US93/09340
; FILING DATE: 30-SEP-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:152/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-468-793-8

Query Match 17.4%; Score 1004.5; DB 3; Length 453;
Best Local Similarity 47.1%; Pred. No. 3.5e-71;
Matches 209; Conservative 72; Mismatches 158; Indels 5; Gaps 3;

QY 12 FKKILVANGETAVRAALETGAATVAIYPREDGSPHRSFASAEVRIGTEGSPVKAY 71

Db 3 FNKILIANGETALRIITCEELGIGTIAVHSTVDNRNALHVLQDAEAVCIG-EAASSKSY 61

QY 72 LDIDEIIGAARKVKADAIYPGYGFLSENAQLARECAENGITITGTPPEVDLTGDKSRV 131

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QY 191 ATEASREAAACDGAIVYVERAVINPOHIEVQILGDHTEGVVHLYERDCSLQRRHKVVE 250

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QY 311 EEVTEVDLYKAQMLAAGATLKLGLTQDKIKTHGAALOCRITTEDPNNNGFRDPTGTIA 370

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RESULT 15
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; Sequence 121, Application US/09433043B
; Patent No. 6399342
; GENERAL INFORMATION:
; APPLICANT: HASSELKORN, ROBERT
; APPLICANT: GORNICKI, PIOTR
; TITLE OF INVENTION: CYANOBACTERIAL AND PLANT ACETYL-CoA CARBOXYLASE
; FILE REFERENCE: ARCD:338US
; CURRENT APPLICATION NUMBER: US/09/433,043B
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 08/475,879
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/956,700
; PRIOR FILING DATE: 1992-10-02
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 121
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-433-043B-121

Query Match 17.3%; Score 1002.5; DB 4; Length 453;
Best Local Similarity 47.1%; Pred. No. 5e-71;
Matches 209; Conservative 72; Mismatches 158; Indels 5; Gaps 3;

QY 12 FKKILVANGETAVRAALETGAATVAIYPREDGSPHRSFASAEVRIGTEGSPVKAY 71

Db 3 FNKILIANGETALRIITCEELGIGTIAVHSTVDNRNALHVLQDAEAVCIG-EAASSKSY 61

QY 72 LDIDEIIGAARKVKADAIYPGYGFLSENAQLARECAENGITITGTPPEVDLTGDKSRV 131

Db 62 LAINPILAAALTNASAIHPGYGFLAENARFAEICADHLLTFIGSPDSIRAMGDKSTAK 121

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OM protein - protein search, using sw model

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications_AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5788	100.0	1140	10	Sequence 19, Appl
3	5788	100.0	1140	15	Sequence 4265, Ap
4	5759	99.5	1157	10	Sequence 2, Appl
5	5759	99.5	1157	10	Sequence 2, Appl
6	2488	43.0	1147	9	US-09-974-973-4
7	2472.5	42.7	1142	9	US-09-815-242-5468
8	2299	39.7	1073	9	Sequence 10806, A
9	1036.5	17.9	447	9	Sequence 12361, A
10	1004.5	17.4	453	9	Sequence 6, Appl
11	976.5	16.9	471	9	US-09-767-479-8
12	957	16.5	449	9	Sequence 5215, Ap
13	946	16.3	448	9	Sequence 13885, A
14	942.5	16.3	455	9	Sequence 11160, A
15	942	16.3	1171	15	US-09-815-242-13617
					Sequence 14226, A

16	941.5	16.3	455	9	US-09-815-242-13364	Sequence 13364, A
17	938	16.2	449	9	US-09-815-242-10330	Sequence 10330, A
18	924	16.0	449	9	US-09-815-242-12063	Sequence 12063, A
19	914	15.8	458	9	US-09-815-242-11321	Sequence 11321, A
20	911	15.7	456	9	US-09-815-242-10924	Sequence 10924, A
21	911	15.7	590	15	US-10-156-761-10874	Sequence 10874, A
22	911	15.7	725	15	US-10-160-501-17	Sequence 17, Appl
23	910	15.7	443	9	US-09-815-242-4963	Sequence 4963, Ap
24	910	15.7	725	15	US-10-224-539A-2	Sequence 2, Appl
25	910	15.7	725	15	US-10-224-539A-9	Sequence 9, Appl
26	905	15.6	590	12	US-10-045-612A-25	Sequence 25, Appl
27	897	15.5	455	9	US-09-815-242-11558	Sequence 11558, A
28	892	15.4	590	12	US-10-045-612A-26	Sequence 26, Appl
29	892	15.4	700	15	US-10-156-761-12811	Sequence 12811, A
30	880.5	15.2	591	10	US-09-738-626-6940	Sequence 6940, Ap
31	859.5	14.8	446	9	US-09-815-242-5418	Sequence 5418, Ap
32	859.5	14.8	453	9	US-09-815-242-12562	Sequence 12562, A
33	840	14.5	448	9	US-09-815-242-5806	Sequence 5806, Ap
34	837	14.5	451	9	US-09-815-242-13127	Sequence 13127, A
35	826.5	14.3	616	15	US-10-156-761-11400	Sequence 11400, A
36	653	11.3	464	15	US-10-169-048-28	Sequence 28, Appl
37	636	11.0	358	9	US-09-815-242-12939	Sequence 12939, A
38	580.5	10.0	2257	9	US-09-767-479-10	Sequence 10, Appl
39	532.5	9.2	2257	12	US-09-839-477-8	Sequence 8, Appl
40	424.5	7.3	483	15	US-10-083-357-1328	Sequence 1328, Ap
41	421.5	7.3	262	15	US-10-224-539A-5	Sequence 5, Appl
42	380.5	6.6	158	9	US-09-815-242-5031	Sequence 5031, Ap
43	301.5	5.2	163	10	US-09-895-913A-324	Sequence 324, Appl
44	255	4.4	1073	16	US-10-210-115-20	Sequence 20, Appl
45	245	4.2	124	9	US-09-205-658-240	Sequence 240, App

ALIGNMENTS

RESULT 1

```

US-09-974-973-19
; Sequence 19, Application US/09974973
; Patent No. US2002017202A1
; GENERAL INFORMATION:
; APPLICANT: Hanke, Paul D.
; TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacter
; FILE REFERENCE: 1533.1230001/MAC/RGM
; CURRENT APPLICATION NUMBER: US/09/974,973
; CURRENT FILING DATE: 2001-10-21
; PRIOR APPLICATION NUMBER: US 60/239,913
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-974-973-19

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Query Match	100.0%	Score 5788;	DB 10;	Length 1140;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1140;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	MSTHTSSTLPAPFKKILVANRGEIAVRAALETGAATVAIYPREDRGSFHRSFASAVR	60	
DB	1	MSTHTSSTLPAPFKKILVANRGEIAVRAALETGAATVAIYPREDRGSFHRSFASAVR	60	
QY	61	IGTESPPKAYLDTDEIIGAACKKADAIYGYGFLSNAQLARECAENGITFTGPTPEV	120	
DB	61	IGTESPPKAYLDTDEIIGAACKKADAIYGYGFLSNAQLARECAENGITFTGPTPEV	120	
QY	121	LDLTGDKSRVTAACKAGLPVLAESTPSKNIDEIVKSAEGOTYPIFYKAVAGGGRGMRF	180	
DB	121	LDLTGDKSRVTAACKAGLPVLAESTPSKNIDEIVKSAEGOTYPIFYKAVAGGGRGMRF	180	
QY	181	VASDELKLTATASREAAAFGDAVYVERAVINPQHIEVOILGDHTGTVVHYERDCS	240	
DB	181	VASDELKLTATASREAAAFGDAVYVERAVINPQHIEVOILGDHTGTVVHYERDCS	240	

Db 181 VASDELKRLATEAREAAFGDGAIVYVERAVINPQHIEVQILGDHTGEVHHLYERDCS 240
QY 241 LQRRHQKVVEIAPAHLDPELRDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEKN 300
Db 241 LQRRHQKVVEIAPAHLDPELRDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEKN 300
QY 301 PRIQVEHTVTEVTEVDLVKAQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNN 360
Db 301 PRIQVEHTVTEVTEVDLVKAQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNN 360
QY 361 PRPDGTITAYRSPGGAGVLDGAALGGEITTAHFDMSLVKMTCRGSDPETAVARAQRAL 420
Db 361 PRPDGTITAYRSPGGAGVLDGAALGGEITTAHFDMSLVKMTCRGSDPETAVARAQRAL 420
QY 421 AEFTVSGVATNIGFLRALLREDEFTSKRIATGFIADHPHLLQAPADDEQGRILDYLDV 480
Db 421 AEFTVSGVATNIGFLRALLREDEFTSKRIATGFIADHPHLLQAPADDEQGRILDYLDV 480
QY 481 TVNKHGVRPKDVAAPIDKLPNIKDLPLPRGSRDLKOLGPAAFARDLREQDALAVTDTT 540
Db 481 TVNKHGVRPKDVAAPIDKLPNIKDLPLPRGSRDLKOLGPAAFARDLREQDALAVTDTT 540
QY 541 FRAHQSLATRVRSFALKPAAEAVAKLTPELLSVEANGGATYDVAMRFLFEDPWRDLDE 600
Db 541 FRAHQSLATRVRSFALKPAAEAVAKLTPELLSVEANGGATYDVAMRFLFEDPWRDLDE 600
QY 601 LREAMPNVNIOMLLRGNTVGYTPYDPSVCRFAFYKEAASSGVDFIPRIFDALNDVSQMRPA 660
Db 601 LREAMPNVNIOMLLRGNTVGYTPYDPSVCRFAFYKEAASSGVDFIPRIFDALNDVSQMRPA 660
QY 661 IDAVLENTVAEVAAMAYSGDLSDPNEKLYLDYLLKMAEETVKSAGHILAIKDMAGLLR 720
Db 661 IDAVLENTVAEVAAMAYSGDLSDPNEKLYLDYLLKMAEETVKSAGHILAIKDMAGLLR 720
QY 721 PAAVTKLVTALRREFDLPHVHTHTAGGLATYFAAAQAGADAVDGAASPLSGTTSOPS 780
Db 721 PAAVTKLVTALRREFDLPHVHTHTAGGLATYFAAAQAGADAVDGAASPLSGTTSOPS 780
QY 781 LSAIVAAFAHRTDGLSLEAVSDLEPYWEAVRGILYLPFESGTPGTGRVYRHEIPGGOL 840
Db 781 LSAIVAAFAHRTDGLSLEAVSDLEPYWEAVRGILYLPFESGTPGTGRVYRHEIPGGOL 840
QY 841 SNLRAQATAGLADRFELIEDNYAAVNMELGRPKYTPSSKVVGDALHLVAGVDPADF 900
Db 841 SNLRAQATAGLADRFELIEDNYAAVNMELGRPKYTPSSKVVGDALHLVAGVDPADF 900
QY 901 AADPKQYDIPDSVIAFLRGELGNPPGWPPEPLRTRALEGRSEKAPLTEVPEEQAHLLDA 960
Db 901 AADPKQYDIPDSVIAFLRGELGNPPGWPPEPLRTRALEGRSEKAPLTEVPEEQAHLLDA 960
QY 961 DDKERRNSLRLLFPKPTTEFLHRRRFGNTSALDREFFYGLVGBGRTILRLPDVTRP 1020
Db 961 DDKERRNSLRLLFPKPTTEFLHRRRFGNTSALDREFFYGLVGBGRTILRLPDVTRP 1020
QY 1021 LLVRDLAISPPDDKGMNVANVNGQIRPMVRDRSVESVTATAEKADSSNKGHVAAPFA 1080
Db 1021 LLVRDLAISPPDDKGMNVANVNGQIRPMVRDRSVESVTATAEKADSSNKGHVAAPFA 1080
QY 1081 GVWTVTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAAATKVEGGDLIVVVS 1140
Db 1081 GVWTVTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAAATKVEGGDLIVVVS 1140

RESULT 2

US-09-738-626-4265
; Sequence 4265, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO

; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent in ver. 3.0
; SEQ ID NO 4265
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4265

Query Match 100.0%; Score 5788; DB 10; Length 1140;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTHTSSILPAPFKKILVANRGEIAVRAPRAALETGAATVAIYPREDRSGFHRSFASEAVR 60
Db 1 MSTHTSSILPAPFKKILVANRGEIAVRAPRAALETGAATVAIYPREDRSGFHRSFASEAVR 60
QY 61 IGTGESSPVKAYIDIDEIIGAARKKADAIYPCYGFSLNSAOLARECAENGTFICPTPEV 120
Db 61 IGTGESSPVKAYIDIDEIIGAARKKADAIYPCYGFSLNSAOLARECAENGTFICPTPEV 120
QY 121 LDLTGDKSRVTAANKAGLPVLAESTPSKNIDEIIVKSAEGOTYPIFVKAVAGGGRGMRF 180
Db 121 LDLTGDKSRVTAANKAGLPVLAESTPSKNIDEIIVKSAEGOTYPIFVKAVAGGGRGMRF 180
QY 181 VASDELKRLATEAREAAFGDGAIVYVERAVINPQHIEVQILGDHTGEVHHLYERDCS 240
Db 181 VASDELKRLATEAREAAFGDGAIVYVERAVINPQHIEVQILGDHTGEVHHLYERDCS 240
QY 241 LQRRHQKVVEIAPAHLDPELRDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEKN 300
Db 241 LQRRHQKVVEIAPAHLDPELRDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEKN 300
QY 301 PRIQVEHTVTEVTEVDLVKAQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNN 360
Db 301 PRIQVEHTVTEVTEVDLVKAQMLAAGATLKEGLTQDKIKTHGAALQCRITTEDPNN 360
QY 361 PRPDGTITAYRSPGGAGVLDGAALGGEITTAHFDMSLVKMTCRGSDPETAVARAQRAL 420
Db 361 PRPDGTITAYRSPGGAGVLDGAALGGEITTAHFDMSLVKMTCRGSDPETAVARAQRAL 420
QY 421 AEFTVSGVATNIGFLRALLREDEFTSKRIATGFIADHPHLLQAPADDEQGRILDYLDV 480
Db 421 AEFTVSGVATNIGFLRALLREDEFTSKRIATGFIADHPHLLQAPADDEQGRILDYLDV 480
QY 481 TVNKHGVRPKDVAAPIDKLPNIKDLPLPRGSRDLKOLGPAAFARDLREQDALAVTDTT 540
Db 481 TVNKHGVRPKDVAAPIDKLPNIKDLPLPRGSRDLKOLGPAAFARDLREQDALAVTDTT 540
QY 541 FRAHQSLATRVRSFALKPAAEAVAKLTPELLSVEANGGATYDVAMRFLFEDPWRDLDE 600
Db 541 FRAHQSLATRVRSFALKPAAEAVAKLTPELLSVEANGGATYDVAMRFLFEDPWRDLDE 600
QY 601 LREAMPNVNIOMLLRGNTVGYTPYDPSVCRFAFYKEAASSGVDFIPRIFDALNDVSQMRPA 660
Db 601 LREAMPNVNIOMLLRGNTVGYTPYDPSVCRFAFYKEAASSGVDFIPRIFDALNDVSQMRPA 660
QY 661 IDAVLENTVAEVAAMAYSGDLSDPNEKLYLDYLLKMAEETVKSAGHILAIKDMAGLLR 720
Db 661 IDAVLENTVAEVAAMAYSGDLSDPNEKLYLDYLLKMAEETVKSAGHILAIKDMAGLLR 720

Db 661 IDAVLENTAFAEYAMAYSGDLPNEKLYTLDYLLKMAEEIVKSGAHILAIDMAGLLR 720
 QY 721 PAAVTKLVTLALRREFDLPVHVHTDTHAGGQATVFAAAQACADAVDASAPLSSTTQPS 780
 Db 721 PAAVTKLVTLALRREFDLPVHVHTDTHAGGQATVFAAAQACADAVDASAPLSSTTQPS 780
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 Db 781 LSAIVAAFAHTRDRTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGQL 840
 QY 841 SNLRAQATLGLADREFLIEDNAAVNEMLGRTKVTPSSKVVGDALHLVAGVDPADF 900
 Db 841 SNLRAQATLGLADREFLIEDNAAVNEMLGRTKVTPSSKVVGDALHLVAGVDPADF 900
 QY 901 AADPOKYDIPDSVIAFLRGELNPPGGWPEPLTRALEGRSEKAPLTPVEPEEQAHLD 960
 Db 901 AADPOKYDIPDSVIAFLRGELNPPGGWPEPLTRALEGRSEKAPLTPVEPEEQAHLD 960
 QY 961 DSKERRNSLNRLFPKPTPEEFLEHRRRFGNTSALDDREFFYGLVGEGRTELIRLPDVRTP 1020
 Db 961 DSKERRNSLNRLFPKPTPEEFLEHRRRFGNTSALDDREFFYGLVGEGRTELIRLPDVRTP 1020
 QY 1021 LLVRLDAISEPDDKGMNVVNVANVNGQIRPMRVDRSVEVTATAEKADSNKGHVAAPFA 1080
 Db 1021 LLVRLDAISEPDDKGMNVVNVANVNGQIRPMRVDRSVEVTATAEKADSNKGHVAAPFA 1080
 QY 1081 GVVTVTVAGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAAATKVEGDLIVVVS 1140
 Db 1081 GVVTVTVAGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAAATKVEGDLIVVVS 1140

RESULT 3
 US-10-045-072-2
 ; Sequence 2, Application US/10045072
 ; Publication No. US20030027305A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sinskey, Anthony J.
 ; APPLICANT: Lessard, Philip A.
 ; TITLE OF INVENTION: Pyruvate Carboxylase from *Corynebacterium glutamicum*
 ; FILE REFERENCE: 1533.0790002
 ; CURRENT APPLICATION NUMBER: US/10/045,072
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR FILING DATE: 1998-12-23
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1140
 ; TYPE: PRT
 ; ORGANISM: *Corynebacterium glutamicum*
 US-10-045-072-2

Query Match 100.0%; Score 5788; DB 15; Length 1140;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTHTSSTLPAPKKILVANRGETAVRAFAALETGAATVAIYIPREDRGSFHRSEFAEVR 60
 Db 1 MSTHTSSTLPAPKKILVANRGETAVRAFAALETGAATVAIYIPREDRGSFHRSEFAEVR 60
 QY 61 IGTGSPVKAYLIDDEIIIGAANKVKADAIYPGYGFLSENAQLARECAENGTIFIGPTPEV 120
 Db 61 IGTGSPVKAYLIDDEIIIGAANKVKADAIYPGYGFLSENAQLARECAENGTIFIGPTPEV 120
 QY 121 LDLTGDKSRAVTAAKAGLPVLAESTPSKNIDEIVKSAEGQYPIFVKAVAGGGGRMF 180
 Db 121 LDLTGDKSRAVTAAKAGLPVLAESTPSKNIDEIVKSAEGQYPIFVKAVAGGGGRMF 180
 QY 181 VASPDRLKLAETASREAAECDCGAVYVERAVINPOHIEVQILGDHTGEVHLYERDCS 240

Db 181 VASPDRLKLAETASREAAECDCGAVYVERAVINPOHIEVQILGDHTGEVHLYERDCS 240
 QY 241 LQRHQKVVETAPAHLDPELRDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFIEMN 300
 Db 241 LQRHQKVVETAPAHLDPELRDRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFIEMN 300
 QY 301 PRIOVEHTVTEEVTEVDLVKAQMLAAGATILKELGLTQDKIKTHGAALQCRITTEDNNG 360
 Db 301 PRIOVEHTVTEEVTEVDLVKAQMLAAGATILKELGLTQDKIKTHGAALQCRITTEDNNG 360
 QY 361 FRPDGTGITAYRSPGGAGVRLDGAALGGGETTAHFDLSMLVKMTCRGSDFFETAVARAQAL 420
 Db 361 FRPDGTGITAYRSPGGAGVRLDGAALGGGETTAHFDLSMLVKMTCRGSDFFETAVARAQAL 420
 QY 421 AEFTVSVATNIGFLRALLREEDFTSKRIATGFTIADHPHLIQAAPPADDEQGRILDLADV 480
 Db 421 AEFTVSVATNIGFLRALLREEDFTSKRIATGFTIADHPHLIQAAPPADDEQGRILDLADV 480
 QY 481 TVNKPCHVRPKDVAAPIDKLPNIKOLPLPRGSRDLKQLGPAAPAFARDLREQDALAVDTT 540
 Db 481 TVNKPCHVRPKDVAAPIDKLPNIKOLPLPRGSRDLKQLGPAAPAFARDLREQDALAVDTT 540
 QY 541 FRDAHOSLLATRVRSFALKAAPAAVAKLTPELLISVEAWGGATYDVAMRFLFEPDWRDLDE 600
 Db 541 FRDAHOSLLATRVRSFALKAAPAAVAKLTPELLISVEAWGGATYDVAMRFLFEPDWRDLDE 600
 QY 601 LREAMPNVNTQMLLRGNTVGYTPYDPSVCRFAVKEAASGVDFIRIFDALNDVDSQMRPA 660
 Db 601 LREAMPNVNTQMLLRGNTVGYTPYDPSVCRFAVKEAASGVDFIRIFDALNDVDSQMRPA 660
 QY 661 IDAVLENTAFAEYAMAYSGDLPNEKLYTLDYLLKMAEEIVKSGAHILAIDMAGLLR 720
 Db 661 IDAVLENTAFAEYAMAYSGDLPNEKLYTLDYLLKMAEEIVKSGAHILAIDMAGLLR 720
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 Db 721 PAAVTKLVTLALRREFDLPVHVHTDTHAGGQATVFAAAQACADAVDASAPLSSTTQPS 780
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 Db 781 LSAIVAAFAHTRDRTGLSLEAVSDLEPYWEAVRGLYLPFESGTPGPTGRVYRHEIPGQL 840
 QY 841 SNLRAQATLGLADREFLIEDNAAVNEMLGRTKVTPSSKVVGDALHLVAGVDPADF 900
 Db 841 SNLRAQATLGLADREFLIEDNAAVNEMLGRTKVTPSSKVVGDALHLVAGVDPADF 900
 QY 901 AADPOKYDIPDSVIAFLRGELNPPGGWPEPLTRALEGRSEKAPLTPVEPEEQAHLD 960
 Db 901 AADPOKYDIPDSVIAFLRGELNPPGGWPEPLTRALEGRSEKAPLTPVEPEEQAHLD 960
 QY 961 DSKERRNSLNRLFPKPTPEEFLEHRRRFGNTSALDDREFFYGLVGEGRTELIRLPDVRTP 1020
 Db 961 DSKERRNSLNRLFPKPTPEEFLEHRRRFGNTSALDDREFFYGLVGEGRTELIRLPDVRTP 1020
 QY 1021 LLVRLDAISEPDDKGMNVVNVANVNGQIRPMRVDRSVEVTATAEKADSNKGHVAAPFA 1080
 Db 1021 LLVRLDAISEPDDKGMNVVNVANVNGQIRPMRVDRSVEVTATAEKADSNKGHVAAPFA 1080
 QY 1081 GVVTVTVAGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAAATKVEGDLIVVVS 1140
 Db 1081 GVVTVTVAGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAAATKVEGDLIVVVS 1140

RESULT 4

US-09-974-973-2
 ; Sequence 2, Application US/09974973
 ; Patent No. US20020177202A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hanke, Paul D.
 ; TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from *Corynebacter*
 ; FILE REFERENCE: 1533.1230001/MAC/RGM
 ; CURRENT APPLICATION NUMBER: US/09/974,973
 ; CURRENT FILING DATE: 2001-10-21

; PRIOR APPLICATION NUMBER: US 60/239,913
 ; PRIOR FILING DATE: 2000-10-13
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 1157
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-09-974-973-2

Query Match 99.5%; Score 5759; DB 10; Length 1157;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1133; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY	1	MSHTSSTLPAPKIIIVANRGEIAVRAALETGAATVAIYPRDRGSHFSFSEAVR	60
Db	18	VSTHTSSTLPAPKIIIVANRGEIAVRAALETGAATVAIYPRDRGSHFSFSEAVR	77
QY	61	IGTEGSPVKAYLDDIIEIGAAKKVKADALYPGVGLSENAQLARECAENGITFIGTPEV	120
Db	78	IGTEGSPVKAYLDDIIEIGAAKKVKADALYPGVGLSENAQLARECAENGITFIGTPEV	137
QY	121	LDLTGDKSRVTAATAKAGLPVLAESTPSKNIDDIYKSAEGQYPIFVKAVAGGGGRMRF	180
Db	138	LDLTGDKSRVTAATAKAGLPVLAESTPSKNIDDIYKSAEGQYPIFVKAVAGGGGRMRF	197
QY	181	VASPDRLKRLATEASREAAAFDGDGAVYVERAVINPQHIEVQILGDTGEVHLERDCS	240
Db	198	VSSPDRLKRLATEASREAAAFDGDGAVYVERAVINPQHIEVQILGDTGEVHLERDCS	257
QY	241	LQRRHOKVVEIAPAOHLDPEDRICADAVKFCRSIGYOGAGTVFELVDEKGNHVFIEMN	300
Db	258	LQRRHOKVVEIAPAOHLDPEDRICADAVKFCRSIGYOGAGTVFELVDEKGNHVFIEMN	317
QY	301	PRIQVEHTVTEVTEVDLVKQMLRAAGATKELGLTQDKIKTHGAALQCRITTEDPNN	360
Db	318	PRIQVEHTVTEVTEVDLVKQMLRAAGATKELGLTQDKIKTHGAALQCRITTEDPNN	377
QY	361	FRPDGTITAYRSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFETAVARAQAL	420
Db	378	FRPDGTITAYRSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFETAVARAQAL	437
QY	421	AEFTVSGVATNIGFRLALREEDFTSKRIATGFIADHPHLLQAPADDEQGRILYDADY	480
Db	438	AEFTVSGVATNIGFRLALREEDFTSKRIATGFIADHPHLLQAPADDEQGRILYDADY	497
QY	481	TVNKPBGVVRPKDVAAPIDKLPNIKDLPLPRGSRDLKQLGPAAFARDLREQDALAVTDIT	540
Db	498	TVNKPBGVVRPKDVAAPIDKLPNIKDLPLPRGSRDLKQLGPAAFARDLREQDALAVTDIT	557
QY	541	FRDAHOSLLATVRSFALKPAEAVALKLTPELLSVEANGGATYDVAMRFLFEDPDWDLDE	600
Db	558	FRDAHOSLLATVRSFALKPAEAVALKLTPELLSVEANGGATYDVAMRFLFEDPDWDLDE	617
QY	601	LREAMPNVIQMLLRNTVGTPTYPDSVCRAVKEAASSGVYDIFRIFDALNDVSMRPA	660
Db	618	LREAMPNVIQMLLRNTVGTPTYPDSVCRAVKEAASSGVYDIFRIFDALNDVSMRPA	677
QY	661	IDAVLETNTVAEAMAYSGDLSDPNEKLYTLDDYLVKMAEIVKSGAHILAIKQAGLLR	720
Db	678	IDAVLETNTVAEAMAYSGDLSDPNEKLYTLDDYLVKMAEIVKSGAHILAIKQAGLLR	737
QY	721	PAAVTKLVALRREFDLPVHVHTHTAGGOLATYFAAQAQADAVDGSAPLSGTTSPS	780
Db	738	PAAVTKLVALRREFDLPVHVHTHTAGGOLATYFAAQAQADAVDGSAPLSGTTSPS	797
QY	781	LSAIVAAFAHTRRDITGLSLEAVSDLEPYWEAVRGLYLPFESCTPGTGRVVRHEIPGGOL	840
Db	798	LSAIVAAFAHTRRDITGLSLEAVSDLEPYWEAVRGLYLPFESCTPGTGRVVRHEIPGGOL	857
QY	841	SNLRAQATGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVAGVDPADF	900
Db	858	SNLRAQATGLADRFELIEDNYAAVNEMLGRPTKVTPSSKVVGDLALHLVAGVDPADF	917

QY	901	AADPOKYDIPDSVIAFLRGLGNPPGWPPELRTALRGRSEKAPLTEVPEEQAHLDA	960
Db	918	AADPOKYDIPDSVIAFLRGLGNPPGWPPELRTALRGRSEKAPLTEVPEEQAHLDA	977
QY	961	DOSKERNLSNRLLPKPTTEEFLEHRRRFRGNTSALDDREFFYGLVEGRETLRLPDVTRP	1020
Db	978	DOSKERNLSNRLLPKPTTEEFLEHRRRFRGNTSALDDREFFYGLVEGRETLRLPDVTRP	1037
QY	1021	LLVRIDAISEPDDKGMNVVNVNGQIRPMVRDRSVESVTATAEKADSSKNGHVAAPFA	1080
Db	1038	LLVRIDAISEPDDKGMNVVNVNGQIRPMVRDRSVESVTATAEKADSSKNGHVAAPFA	1097
QY	1081	GVVTVTVAGDEVKAGDAVAIIEAMKMEATIASVDGKIDRVVVPAAATKVEGGDLIVVYS	1140
Db	1098	GVVTVTVAGDEVKAGDAVAIIEAMKMEATIASVDGKIDRVVVPAAATKVEGGDLIVVYS	1157

RESULT 5

US-09-974-973-4
 ; Sequence 4, Application US/09974973
 ; Patent No. US20020177202A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hanke, Paul D.
 ; TITLE OF INVENTION: Feedback-Resistant Pyruvate Carboxylase Gene from Corynebacter
 ; FILE REFERENCE: 1533.1230001/MAC/RGM
 ; CURRENT APPLICATION NUMBER: US/09/974,973
 ; CURRENT FILING DATE: 2001-10-21
 ; PRIOR APPLICATION NUMBER: US 60/239,913
 ; PRIOR FILING DATE: 2000-10-13
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 1157
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-09-974-973-4

Query Match 99.5%; Score 5759; DB 10; Length 1157;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1133; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY	1	MSHTSSTLPAPKIIIVANRGEIAVRAALETGAATVAIYPRDRGSHFSFSEAVR	60
Db	18	VSTHTSSTLPAPKIIIVANRGEIAVRAALETGAATVAIYPRDRGSHFSFSEAVR	77
QY	61	IGTEGSPVKAYLDDIIEIGAAKKVKADALYPGVGLSENAQLARECAENGITFIGTPEV	120
Db	78	IGTEGSPVKAYLDDIIEIGAAKKVKADALYPGVGLSENAQLARECAENGITFIGTPEV	137
QY	121	LDLTGDKSRVTAATAKAGLPVLAESTPSKNIDDIYKSAEGQYPIFVKAVAGGGGRMRF	180
Db	138	LDLTGDKSRVTAATAKAGLPVLAESTPSKNIDDIYKSAEGQYPIFVKAVAGGGGRMRF	197
QY	181	VASPDRLKRLATEASREAAAFDGDGAVYVERAVINPQHIEVQILGDTGEVHLERDCS	240
Db	198	VSSPDRLKRLATEASREAAAFDGDGAVYVERAVINPQHIEVQILGDTGEVHLERDCS	257
QY	241	LQRRHOKVVEIAPAOHLDPEDRICADAVKFCRSIGYOGAGTVFELVDEKGNHVFIEMN	300
Db	258	LQRRHOKVVEIAPAOHLDPEDRICADAVKFCRSIGYOGAGTVFELVDEKGNHVFIEMN	317
QY	301	PRIQVEHTVTEVTEVDLVKQMLRAAGATKELGLTQDKIKTHGAALQCRITTEDPNN	360
Db	318	PRIQVEHTVTEVTEVDLVKQMLRAAGATKELGLTQDKIKTHGAALQCRITTEDPNN	377
QY	361	FRPDGTITAYRSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFETAVARAQAL	420
Db	378	FRPDGTITAYRSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFETAVARAQAL	437
QY	421	AEFTVSGVATNIGFRLALREEDFTSKRIATGFIADHPHLLQAPADDEQGRILYDADY	480
Db	438	AEFTVSGVATNIGFRLALREEDFTSKRIATGFIADHPHLLQAPADDEQGRILYDADY	497

QY 481 TVNKHGVRKDVAAPIKLPNIKDLPLPGSRDLKOLGPAFAFARDLREODALAVDTT 540
 Db 498 TVNKHGVRKDVAAPIKLPNIKDLPLPGSRDLKOLGPAFAFARDLREODALAVDTT 557
 QY 541 FRDAHQSLLATRVRSFALKPAAEAVALTPELLSVEAMGGATYDVAMREFLFEDEPWRDLDE 600
 Db 558 FRDAHQSLLATRVRSFALKPAAEAVALTPELLSVEAMGGATYDVAMREFLFEDEPWRDLDE 617
 QY 601 LREAMPNVNOMLGRNTVGYTPYPDSVCRFAFKEAASSGVDIFRFDALNDVDSQMRPA 660
 Db 618 LREAMPNVNOMLGRNTVGYTPYPDSVCRFAFKEAASSGVDIFRFDALNDVDSQMRPA 677
 QY 661 IDAVLENTAVAEVAMAYSGDLSDPNEKLYTLDYLLKMAEEIVKSGAHILAIDMAGLLR 720
 Db 678 IDAVLENTAVAEVAMAYSGDLSDPNEKLYTLDYLLKMAEEIVKSGAHILAIDMAGLLR 737
 QY 721 PAAVTKLVTALRREFDLPVHVHTDTAGGQIATYFAAAQAGADAVDGCASAPLSGTTSQPS 780
 Db 738 PAAVTKLVTALRREFDLPVHVHTDTAGGQIATYFAAAQAGADAVDGCASAPLSGTTSQPS 797
 QY 781 LSAIVAAFAATRTDGLSLEAVSDLEPYWEAVRGLXLPFESGTPGPTGRVYRHEIPGGQL 840
 Db 798 LSAIVAAFAATRTDGLSLEAVSDLEPYWEAVRGLXLPFESGTPGPTGRVYRHEIPGGQL 857
 QY 841 SNLRAQATLGLADRFELIEDNYAAVNEMLGRPTKVPSSKVVGDLALHLVAGVDPADF 900
 Db 858 SNLRAQATLGLADRFELIEDNYAAVNEMLGRPTKVPSSKVVGDLALHLVAGVDPADF 917
 QY 901 AADPOKYDIPDSVIAFLRGELNPPGGWPEPLKTRALRGRSEKAPLTVPEEQAHLDA 960
 Db 918 AADPOKYDIPDSVIAFLRGELNPPGGWPEPLKTRALRGRSEKAPLTVPEEQAHLDA 977
 QY 961 DDSKERNSLNRLFPKPTFEFLHRRRFGNTSALDDREFFYGLVGEFTLRLPDVTRP 1020
 Db 978 DDSKERNSLNRLFPKPTFEFLHRRRFGNTSALDDREFFYGLVGEFTLRLPDVTRP 1037
 QY 1021 LLVRLDAISPPDKGMRNVVANYNGQIRPMRVDRDSVESYATAEKADSSNKGHVAAPFA 1080
 Db 1038 LLVRLDAISPPDKGMRNVVANYNGQIRPMRVDRDSVESYATAEKADSSNKGHVAAPFA 1097
 QY 1081 GVVTVTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAAATKVEGGDLIVVVS 1140
 Db 1098 GVVTVTVAEGDEVKAGDAVAIIEMKMEATITASVDGKIDRVVVPAAATKVEGGDLIVVVS 1157

RESULT 6

US-09-815-242-5468
 ; Sequence 5468, Application US/09815242
 ; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: ELITRA.011a
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: PastSeq for Windows Version 4.0
 ; SEQ ID NO 5468
 ; LENGTH: 1147
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-815-242-5468

Query March 43.0%; Score 2488; DB 9; Length 1147;
 Best Local Similarity 45.2%; Pred. No. 1.5e-130;
 Matches 527; Conservative 192; Mismatches 384; Indels 62; Gaps 14;

QY 13 KKLIVANRGETAVRAFAALETGAATVAIYPREDGRSFHRSFSAEAVRIGCTEGSPVKAYL 72
 Db 4 KKLIVANRGETAVRAFAALETGAATVAIYPREDGRSFHRSFSAEAVRIGCTEGSPVKAYL 63
 QY 73 DIDEIIGAAGKVKADAIYPGYGFLSENAQALRECAENGITTFIGPTPEVLDTLTDGKSRVAT 132
 Db 64 NIERLIDVAQANVDALHPGYGFLSENEQFARRCAEBGKIFGPHLEHDMFGDKVKART 123
 QY 133 AAKKAGLPVL-ABSTPSKNIDEIVKSEAGQYPIFYKAVAGGGGGRMRFVASDPDELKLA 191
 Db 124 TALKADLPVTPGTGPIKSYELAKEFAEEAGFPLMIKATSGGGKGMRIYRESEDEDAF 183
 QY 192 TEASREAAAFAGDGVAVYVERAVINPOHIEVOILGDHTGEVYVHYLYERDCSLQRHOKVVEI 251
 Db 184 HRAKSEAKSFGSENVYIERIDNPKHIEVOVIGDEHGNIVHLFERDCSVQRHOKVVEI 243
 QY 252 APAQLHLDPELRDICAADVCFKCSIGYQGAGTVEFLV--DEKGNHVEIEMNPRIQVEHTV 309
 Db 244 APSVGLSPILRQICDAAIQLMENIKYVNAGTVEFLVSGDE---FFIEVNPVQVEHTI 300
 QY 310 TEETVEVDLVKAOMLAAGATL--KELGLTQDK-IKTHGAALQCRITTEDPNNNGFRPDGT 366
 Db 301 TEMVTGIDIVTKTQILVAAGADLFGEEINMPQKDDITTLGYAIOCRITTEDPNDENFMDTG 360
 QY 367 TITAYRSPGAGVRLD-GAAQLGGEITAHFDSMLVKMTCRGDSFETAVARAQALAEFTV 425
 Db 361 TITAYRSGGFGVRLDAGDGFQGAIEISPYDLSLLVLKSTHAIASFQAEKRWLSREMRI 420
 QY 426 SGVATNIGFLRALLREEDFTSKRIATGFIADPHLLOAPPADDEQGRILDYLDADVTKNP 485
 Db 421 RGVKTNIPFLINVMKMKFTSGDYTKFTIETPELEFIQPSLDRGKTKLEYIGNVTIN-- 478
 QY 486 HGVRPKDVAAPIDKLPNIKDLPLP-----RGSRLKOLGPAFAAFARD 527
 Db 479 -----GFTNVEKRKPKDYELASIPVSSSKTASFSGTQKLLDEVGPKGVAEW 525
 QY 528 LREQDALAVTDTTFRDAHQSLLATRVRSFALKPAAEAVAKLTPELLSVEAMGGATYDVAM 587
 Db 526 VKKQDDVLLTDTTFRDAHQSLLATRVRTKDMINIAASKTADVFVKDGSFLEAMGGATFDVAY 585
 QY 588 RLTFEDPPWRDLDELREAMPNVNQLLRGNNTVGYTPYPDSVCRFAFKEAASSGVDIFRI 647
 Db 586 NFLKENPWERLERKRAIPNVLFQMLLRASNAGVYKKNYKPNVTHKVEQVSAKAGIDVFR 645
 QY 648 FDALNDVSQMRPAIDAVLETNTAVAEVAMAYSGDLSDP-NEKLYTLDYLLKMAEEIVKSG 706
 Db 646 FDSLNNVDQMKVANAEOVQAG-KISEGTICYTGDIINPERSNIYLEYVYVKKLAKELEREG 704
 QY 707 AHILAIDKMAGLLRPAATVKLVIALRRREFDLPVHVHTDTAGGQIATYFAAAQAGADAVD 766
 Db 705 FHILAIDKMAGLLKPKAAAYELIGELKAAVLDPLHLHTHTDTSNGLLTYKQADAGVDIID 764
 QY 767 GASAPLSGTTSQPSLSAIVAAFAHTRRTDGLSLEAVSDLEPYWEAVRGLXLPFESGTPGP 826
 Db 765 TAVASMSGTTSQPSANSLYALNGFPRLRTRTDIEGMESLSHYWSTVRYTYSDFESDIKSP 824

[illegible]

RESULTS

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US-09-815-242-10806
; Sequence 10806, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/131,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10806
; LENGTH: 1142
; TYPE: PR1
; ORGANISM: Enterococcus faecalis
US-09-815-242-10806

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[illegible]


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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/767,479
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: Unknown
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/468,793
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; APPLICATION NUMBER: PCT/US93/09340
; FILING DATE: 30-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:152/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-767-479-6

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Query Match 17.9%; Score 1036.5; DB 9; Length 447;
Best Local Similarity 48.4%; Pred. No. 1.3e-74;
Matches 216; Conservative 73; Mismatches 152; Indels 5; Gaps 3;

QY 12 FKKILVANRGEIIVAFRAALETGAATVAIYPRDRGSHFRSFAEAVRIGTEGSPVKAY 71
Db 3 FDKILIANRGETALRILRACEEMGIATIAVHSTVDNHALVQLADEAVCIG-EPASAKY 61

QY 72 LDIDEIICAANKVADAIYPGVGFSENAQLARECAENGITFPTPEVLDITGDKSRV 131
Db 62 LNIPIIAAALTRNASAIHPGYGFLAENARFAEICADHHLIFIGPSPSIRAMGDKSTAK 121

QY 132 TAAKAGLPLVLAESTPP-SKNIDEIVKSAEGOTYPIFVKAVAGGGGRMRVFPDELRL 190
Db 122 ETMQAGVTPVPGSGLVETQEGLELANDIGYPMIKATAGGGGRGMRVSPDEFVKL 181

QY 191 ATEASREAEAFGDGAVYVERAVINPQIHIEVQILGDHTGEVYVHLVYERDCSLORRHQKVE 250
Db 182 FLAQQEAGAAFGNAGVYIERPRHIEFQILLADNYGNVHLGERDCSIQRRNQKLE 241

QY 251 IAPQHLDELDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEMNPRIOVEHVT 310
Db 242 EAPSPALDSUREKMGQAQAAQOPIYNTGAGTIEFLDRSGQFYFMEINRIQVEHVT 301

QY 311 EEVTEVDLVKAQMLAAGATLQKLTQDKIKTHGAALQCRITTEDPNNRFPDPTGTTA 370
Db 302 EMVTGVDLLVEQIRTAQGERLUR---LTQDQVVLGRHGAIECRINAEDPDHDFPAPCRISG 358

QY 371 YRSPGCGVRLDGAALQGEITAHFDSMLVKMTCRGSDFETAVARAQALAEFTVSGVAT 430
Db 359 YLPPGPGVGRIDSHVYTYDQIPPPYDLSLKLIVNGPDRATAINRMKRALRECAITGLPT 418

QY 431 NIGELRALLREDDFTSKRIATCFIAD 456
Db 419 TIGFHQRIMENPQFLQGNVSTSFVOE 444

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RESULT 10

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US-09-767-479-8
; Sequence 8, Application US/09767479
; Patent No. US200100366541
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert

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; Gornicki, Piotr
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/767,479
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: Unknown
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/468,793
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; APPLICATION NUMBER: PCT/US93/09340
; FILING DATE: 30-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:152/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-767-479-8

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Query Match 17.4%; Score 1004.5; DB 9; Length 453;
Best Local Similarity 47.1%; Pred. No. 5.1e-72;
Matches 209; Conservative 72; Mismatches 158; Indels 5; Gaps 3;

QY 12 FKKILVANRGEIIVAFRAALETGAATVAIYPRDRGSHFRSFAEAVRIGTEGSPVKAY 71
Db 3 FDKILIANRGETALRILRACEEMGIATIAVHSTVDNHALVQLADEAVCIG-EAASSKY 61

QY 72 LDIDEIICAANKVADAIYPGVGFSENAQLARECAENGITFPTPEVLDITGDKSRV 131
Db 62 LNIPIIAAALTRNASAIHPGYGFLAENARFAEICADHHLIFIGPSPSIRAMGDKSTAK 121

QY 132 TAAKAGLPLVLAESTPP-SKNIDEIVKSAEGOTYPIFVKAVAGGGGRMRVFPDELRL 190
Db 122 ETMQAGVTPVPGSGLVETQEGLELANDIGYPMIKATAGGGGRGMRVSPDEFVKL 181

QY 191 ATEASREAEAFGDGAVYVERAVINPQIHIEVQILGDHTGEVYVHLVYERDCSLORRHQKVE 250
Db 182 FLAQQEAGAAFGNAGVYIERPRHIEFQILLADNYGNVHLGERDCSIQRRNQKLE 241

QY 251 IAPQHLDELDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEMNPRIOVEHVT 310
Db 242 EAPSPALDSUREKMGQAQAAQOPIYNTGAGTIEFLDRSGQFYFMEINRIQVEHVT 301

QY 311 EEVTEVDLVKAQMLAAGATLQKLTQDKIKTHGAALQCRITTEDPNNRFPDPTGTTA 370
Db 302 EMITGLDLIAEQIRTAQGERLUR---FRQADQLGRHGAIECRINAEDPEYFNPRPGRITG 358

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QY 371 YRSPGGAGVRLDGAQAQAGGTAHFDMSLVKMTCRGSDFFETAVARAQALAEFTVSGVAT 430
 Db 359 YLPPGGGVRVDVSHVYDYETPPYDYSGLIGKLIWVGATREAIARMQALRECAITGLPT 418
 QY 431 NIGFLRALLREEDFTSKRIATGFI 454
 Db 419 TLSFHQLMQLQMPFLRGELITNFV 442

RESULT 11

US-09-815-242-5215
 ; Sequence 5215, Application US/09815242
 ; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242
 ; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-05-23

; PRIOR FILING DATE: 2000-05-23

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-10-23

; PRIOR FILING DATE: 2000-11-27

; PRIOR FILING DATE: 2000-12-22

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5215

; LENGTH: 471

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-815-242-5215

Query Match 16.9%; Score 976.5; DB 9; Length 471;
 Best Local Similarity 45.7%; Pred. No. 9.7e-70;
 Matches 208; Conservative 73; Mismatches 159; Indels 15; Gaps 5;

QY 13 KKILVANRGEIAVRAFAALETGAATVAIYPREDGRSFHRSFASAVRIGTEGSPKAYL 72
 Db 3 KKILIANRGEIAVIRVCAEMGIRSVAYSADRHALLVKKRADEAHSIGAD--PLAGYL 60
 QY 73 DIDEIIGAARKVKADAIYPGYFLSNAQALRECAENGITFICPTPEVLDLTGDKSRVAT 132
 Db 61 NPLALVNLAVERGCDALHPGYFLSNAELAEICAERGIKFIGPSAQVIRMGDKTEARR 120
 QY 133 AAKKAGLPVLAESTPS-----KNIDEIVKSAEQYPIPVKAVAGGGGGRMFVAPDEL 187
 Db 121 SMAAGVP---CTPGTEGNVADLAELAEALREAEIRIGYPMVKATSGGGGGRIRCRNSREL 176
 QY 188 RKLATEASREAAFGDGAIVYVERAVINPOHTEVOILGDHGTGEVHLVYERDCSLORRHO 247
 Db 177 EQAFPRVISEATKAFSAEVEFLEKLVNPKHLEAQILADSGFNTVHLFERDCSIQRRNO 236
 QY 248 VVEIAPAHLDPELDRICADAVKFCRSIGYOGAGTVEFLVDEKGNHVFIEIEMNPRIQVEH 307
 Db 237 LIEIAPSPQLTPEQRAYIGDLAVRAAKAVGYENAGTVEFLIAD-GEVYFEMENRIVQVEH 295

QY 308 TVTEEVTEVLDLVKAQMRLAAGATLKGELGTQDKIKTHGAALQCRITTEDPNNRPPDGT 367
 Db 296 TITEIIGIDVVRQIRIASGL--ELSVKODDVIHRYALQFRINADDPKNNFLPSFGK 352
 QY 368 ITAYRSPGGAGVRLDGAQAQAGGTAHFDMSLVKMTCRGSDFFETAVARAQALAEFTVSG 427
 Db 353 ITRYAPGGPGVRTDTAIYGTYTIPPYYDSMCLLIWVWALTWEEALDGLALDDMRVQG 412
 QY 428 VATNIGFLRALLREEDFTSKRIATGFIADHPHLIQ 462
 Db 413 VKTTAPYQETILRNPEFRSGQFNFSVESHPELTQ 447

RESULT 12

US-09-815-242-13885
 ; Sequence 13885, Application US/09815242
 ; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-05-23

; PRIOR FILING DATE: 2000-05-26

; PRIOR FILING DATE: 2000-10-23

; PRIOR FILING DATE: 2000-11-27

; PRIOR FILING DATE: 2000-12-22

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13885

; LENGTH: 449

; TYPE: PRT

; ORGANISM: Salmonella typhi

US-09-815-242-13885

Query Match 16.5%; Score 957; DB 9; Length 449;
 Best Local Similarity 47.6%; Pred. No. 3.3e-68;
 Matches 206; Conservative 61; Mismatches 158; Indels 8; Gaps 5;

QY 14 KILVANRGEIAVRAFAALETGAATVAIYPREDGRSFHRSFASAVRIGTEGSPKAYLD 73
 Db 4 KIVIANRGEIALRILRACKELGKTVAVHSSADRLKHLVLADETVICIGAPPS-VKSYLN 62
 QY 74 IDEITIGAARKVKADAIYPGYFLSNAQALRECAENGITFICPTPEVLDLTGDKSRVAT 133
 Db 63 IPALISAREITCAVAIHFGYFLSNAFPAEVEKSGFIFIGPKADTIRKMGDKVSAITA 122
 QY 134 AKKAGLPVLAESTPSKNIDEIVKSAEQGT--YPIFVKAVAGGGGGRMFVAPDELIRKLA 191
 Db 123 MKKAGVTPVPGSDGPLGDDMMANRAHAKRIGYPIVIAKSGGGGGRMVRVRSDAELAQSI 182
 QY 192 TEASREAAFGDGAIVYVERAVINPOHTEVOILGDHGTGEVHLVYERDCSLORRHO 251
 Db 183 SMTKAEAKAFAFSDNMVYMEKYLENPRHTEIQVLADGOGNAIYLAERDCSGMORRHOKVVEE 242

QY 252 APAQHLDPELRICADAVKFCRSIGYQAGTVEFLVDEKGNHVFTEMNPRIOVEHTVTE 311
 Db 243 APAPGITPELRIRYIGERCACACVDIGYRGAGTFFLF-ENGEBFYTEMNTRIOVEHPVTE 301
 QY 312 EYTEVDLVKAQMLAAGATLKGELGTQDKIKTHGAALOCRIITTEPNNGFRDPTGTITAY 371
 Db 302 MITGVDLKEQIRIAG---QPLSIQDVEVVRGHAVERKINAEEDNT-FLSPGKIRTF 357
 QY 372 RSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFETAVARAQRAIAEFTVSGVATN 431
 Db 358 HAPGGFGVWESHIVAGTYVPPYDYSMICKLICGENRDAIARMKNALQELIIDGIKN 417
 QY 432 IGFRLALLREEDF 444
 Db 418 IDIQTRIMNDEHF 430

RESULT 13

US-09-815-242-11160

; Sequence 11160, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Karl L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR FILING DATE: 2000-03-21

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; PRIOR FILING DATE: 2000-03-21

QY 191 ATEASREAAAFGDGAVYVERAVINPOHLEVOILGDHTGEVHLVYERDCSLORRHOKVVE 250
 Db 182 IAMTRAEAKAANNNDVYMEKYLENPRHVEIQVLADTHGNVLAERDCSMQERHOKVVE 241
 QY 251 IAPAHLDPELRDRI---CADAVKFCRSIGYQAGTVEFLVDEKGNHVFTEMNPRIOVEH 307
 Db 242 EAPAPGITEVERDRIIGSRCANA---CVEIGYRGAGTFFLY-ENGEBFYTEMNTRIOVEH 297
 QY 308 TYTEEVTEVDLVKAQMLAAGATLKGELGTQDKIKTHGAALOCRIITTEPNNGFRDPTGT 367
 Db 298 PVTMITGVLDLKEQIRIAGL---PISFKQEDIKVKGHAMECRINAEDPKT-FLSPGK 353
 QY 368 ITAYRSPGAGVRLDGAALGGEITAHFDSMLVKMTCRGSDFETAVARAQRAIAEFTVSG 427
 Db 354 VNELHSPGGLGVWRDWSHVYGVTPPHYDYSMAKLITYGDTREVAIRRMQNALSETIIDG 413
 QY 428 VATNIGFLRALLREEDF 444
 Db 414 INTNIPHLHELEEDNF 430

RESULT 14

US-09-815-242-13617

; Sequence 13617, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Karl L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

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; PRIOR FILING DATE: 2000-03-21

Query Match 16.3%; Score 942.5; DB 9; Length 455;
 Best Local Similarity 46.0%; Pred. No. 5e-67;
 Matches 206; Conservative 75; Mismatches 160; Indels 7; Gaps 5;

QY 12 FKKILVANRGEIATVAFRAALETGAATVATVYIPREDGRSFHRSFASAVRIGTESPVKAY 71
 Db 2 FRKILVANRGEIATVAFRAALETGAATVATVYIPREDGRSFHRSFASAVRIGTESPVKAY 60
 QY 72 LDIDELIGAAKKVADATVPGYGLFSENAQALARECAENGITFPGTPEVLDLTGDKSRAY 131
 Db 61 LKNVANSAVLTAEAIHPGFGFLSENSKATMCEVGIKFGIPSGHVMDMGDKINAR 120

Query Match 16.3%; Score 946; DB 9; Length 448;
 Best Local Similarity 47.6%; Pred. No. 2.5e-67;
 Matches 208; Conservative 61; Mismatches 154; Indels 14; Gaps 7;

QY 13 KKLIVANRGEIATVAFRAALETGAATVATVYIPREDGRSFHRSFASAVRIGTESPVKAYL 72
 Db 3 EKVIVANRGEIATVAFRAALETGAATVATVYIPREDGRSFHRSFASAVRIGTESPVKAYL 61
 QY 73 DIDEIIGAAKKVADATVPGYGLFSENAQALARECAENGITFPGTPEVLDLTGDKSRAY 132
 Db 62 NIPALIAAAEVTGADAIHPGFGFLSENAQALARECAENGITFPGTPEVLDLTGDKSRAY 121
 QY 133 AAKKAGLPVL--AESTPSKNIDEIVKSAEGOTYPIFVKAVAGGGGGRGMRVFASPDRLKL 190
 Db 122 AMKAGVPCVFGSDGVPVSNDAKNEIAKRIKGYPIIKASGGGGGGRGMRVRSSEDALES 181

QY 132 TAACKAGLPVLAESTPS-KNIDEIVKSAEGQTYPIFKAVAGAGGGGRMRFFVASPELRLK 190
 Db 121 AQMTKAGVPVTPGSDGEVHNSEEAIIAIAKIGYPMVKASAGGGKIRKVEKPPDLVSA 180
 QY 191 ATEASREAAAFGDAVVERAVINPOHIEVQIIGDHTGEVHLYERDCSLQRHQKVE 250
 Db 181 FETASSAKANYGNGAMVIERVYPARHIEVQIIGDHTGEVHLYERDCSLQRNNQKYLE 240
 QY 251 IAPAQHLDPELRDCAVAKFCRSIGYQAGTVEFLVDE-KGNHVFIEMNPRIQVEHTV 309
 Db 241 ESPSIAIGKTLRHEIGAANAFAEFGVENAGTIEFLDDEASSNFYFWMNTRVQVEHPV 300
 QY 310 TEEVTEVDLYKAQMLAAGATLKELGTQDKINKTHGAALOCRIITPDNNGFRPDGTIT 369
 Db 301 TEFVSGVDIVKEQICIAAG--QPLSVKQEDIVLRGHAIECRINAENPAFNAPSPGKIT 357
 QY 370 -AYRSPGGAGVRLDGAALQGEIITAFHDSMLVKMTCRGSDEFETAVARAQALAEFTVSGV 428
 Db 358 NLILPSCGVLRVDSAVYPGVTPPYDYDSMAKIIIVHGENRFDALMKMORALYELEIEG 417
 QY 429 ATNIGFLRALLREDFTSKRATGFIAD 456
 Db 418 QTNADFOLDLISDRNVITAGDYDTSFLME 445

RESULT 15

US-10-156-761-14226
 ; Sequence 14226, Application US/10156761.
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 14226
 ; LENGTH: 1171
 ; TYPE: PRF
 ; ORGANISM: Streptomyces avermitilis
 US-10-156-761-14226

Query Match 16.3%; Score 942; DB 15; Length 1171;
 Best Local Similarity 28.1%; Pred. No. 2.6e-66;
 Matches 368; Conservative 145; Mismatches 471; Indels 326; Gaps 44;
 QY 12 PKILVANGETAVRAFRALLETGAATVAIYPREDGRSPHRSFASAVRIGTEGSPVK-A 70
 Db 3 FDTLLVANGETAVRIVRTARELGLRTAVVSDPDRSAPHVRLADEAVRLGP--APAKES 60
 QY 71 YLDIDIEIGAACKVKADATYPCGYFSENAQLARECAENGIFIGTPTVLDTGDKSRA 130
 Db 61 YLDADLVLAAKDTGAGALHPGYFSEDAARFARCEADAGIVFGTPTQLELFGAKHTA 120
 QY 131 VTAACKAGLPVLAESTPSKNIDEIVKSAEGQTYPIFKAVAGAGGGGRMRFFVASPELRLK 190
 Db 121 RAAAEAAAGVPLAPGTIGLLASLDEALDAASRIGYPMVKATGGGGIGMSACRSALAEAS 180
 QY 191 ATEASREAAAFGDAVVERAVINPOHIEVQIIGDHTGEVHLYERDCSLQRHQKVE 250
 Db 181 WERVRVTAAPSSAGIFLERLVEHARHVEVQVFGDGRGVVTLGDRDCSLQRNQKVE 240
 QY 251 IAPAQHLDPELRDCAVAKFCRSIGYQAGTVEFLVDE-EKGNHVFIEMNPRIQVEHTV 309

Db 241 EAPFGLPSHVRDHLASARDLCRAAGYRSAGTVEFYDAAKEEAYFLEVTRLQVEHPV 300
 QY 310 TEEVTEVDLYKAQMLAAGATLKELGTQDKINKTHGAALOCRIITPDNNGFRPDGTIT 369
 Db 301 TEEYGVDLVAMWLRLAGG---DADVVRDPGPPRGHAEVAVYAEDESRHRFSAGLIT 356
 QY 370 AYRSPGGAGVRLDGAALQGEIITAFHDSMLVKMTCRGSDEFETAVARAQALAEFTVSGV 429
 Db 357 RVEFP--QGVYVDGWVETGTEVTSYDPMALKVAVAYGSDRAHARLALDEALARTVDGIE 414
 QY 430 TNICFLRALLREDFTSKRATGFIAD 456
 Db 415 TNLGLVRAALADHGLRTATHTATLAKITDTPRVVVAAGTTLTVODMPORTGYWQGV 474
 QY 461 LQAPPADD-----EQGR-----ILDYADVTVNPKPHG 487
 Db 475 PPCGPMDDRSFRLGNRALGNEEGAPGLECLTLRGALPALTHTATVYVTCGAPAPVTDGTPV 534
 QY 488 VRPKDVAAPIDKL-----PNIKDLPLRGSRDRLKQLGPAAP-----ARDLR 529
 Db 535 AQWEPVTPPAGALLEVGAPAPGLRTYVLFAGGLDVPALFGLSAATFTLGRFGHGGRALR 594
 QY 530 EODALAVTDITFRDA-----HOSLLATRVRSFALKPAAEAVAKLTPELLSVEAMGGATYD 584
 Db 595 TGDVLHGGSVTDRCAPVPAGDRPVFATEWHVHGALEGHAAPEFFED--DIRDYAAGWK 652
 QY 585 V-----AMRFLFEDP-WDRDLDELREAMPNVNIQMLLRGNTVGYT---PY---PDS-- 628
 Db 653 VHFNSARTGVRLVGPKEPRWARSOGGEAGLHPSNIHDTYPSVGAVDYTGDMFVLLGPDPGS 712
 QY 629 ---VCRAFYKEAASSGVDFRFDALNDVQSRPAIDAVLENTAVAEVAMAYSGDLSD 684
 Db 713 LGGFVCPATVATAERW-----KLGOLRPG-DTVRYT----- 742
 QY 685 PNEKLYTLYLKNABEIVKSGAHILAIKDMAGLLRPAAYT-----KLVTALREFD 736
 Db 743 -----PLAEDGSTREAIYDGGVLRDGDVYRSGDDNLLVFEFGMOLD 786
 QY 737 LPVHVHTHTAGQLATYFAAAQAGADAV-----DGASAPLSGTTSPFSL 782
 Db 787 LALMRVH-----ALMEAVAEAGLDGVDTLFPGIRSLQIRTDPRRLPLR-----ELL 833
 QY 783 AIVAAFAHTERRDTGLSLEAVSDLEPYWEAV---RGLYLPESGTPGTGRVYRHEIPGQ 839
 Db 834 AVVR-----ETVSALPTDQLVVPRTVHLPLSWDDPATRAIERY----- 874
 QY 840 LSNLRAQA-----TALGLADRFELIEDNYAAVNE---MLGRPTKVTSSKVVWGDLAL 888
 Db 875 MAGVRDDAPWCWNIEFIRRVNGLESVADYDVFDAEYVLG-----LGDVYL 923
 QY 889 HLVGAGVDPADFAADPQ-----KYDIPDSVIAFLRNGELNP-----PGWPEPLR 933
 Db 924 ---GA---EVATPLDPRHLRTVTKYNPARTAENSIGGAYLVCYVGMGPGGYQFVGK 977
 QY 934 TRALEGRSEKAPLIEVPEEQAHLDADDKERRNSLNLLPKPTEEFLEHRRRFGNTS 993
 Db 978 T-----TQVWSGW-----ORGAF-----EPGSPWL---LAF--- 1001
 QY 994 ALDDREFFVGLVEGRETLRL--PDVTRTPLLRLDAISEPDDKGRNVVANVNGQLRPMHV 1052
 Db 1002 ---FDRIKWYAV--GPDELLDLRADIASGRFVRVEGEFSLAGYESFLAANAGSAAFA 1057
 QY 1053 R-----DRSVESVTATAKASUSNKGHVAAAFAGVVT-----VTVAG 1090
 Db 1058 ROGAFAAERDAWEAAGEFAFAAATAPEAPPAYEIVTPVVGALVBAEFAAASVWQNLVSPG 1117
 QY 1091 DEVKAGDAVAITEAMKMEATITASVDGKIDRVVPAATKVEGGDLIVVVS 1140
 Db 1118 DAVTAGQPLLTLEAMKMSRVPAPNAGVVVTEILARPGDQVAAAGTALVILA 1167

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Thu Sep 25 08:53:47 2003

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